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OM protein - protein search, using sw model

Run on: May 20, 2002, 09:21:15; Search time 11.88 Seconds (without alignments) 355.255 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-754-826-2 628

Searched:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

1 DFGLDCDEHSTESRCCRYPL.....KEQIIYGKIPAMVVDRCGCS 109

Total number of hits satisfying chosen parameters: 105224

105224 seqs, 38719550 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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Query Match

99.0%; Score 622; DB 1; Length 375;

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## ALIGNMENTS

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EMBL; AF019621; AAB86 HSSP; P18075; 1BMP, InterPro; IPR0011839; InterPro; IPR001111; Pfam; PF00019; TGF-be Pfam; PF00019; TGF-be Pfam; PF0000357; TGF SMART; SM00204; TGFB; PROSTE; PS00250; TGF; Growth factor; Cytoki; SIGNAL 1 2 PROPEP 24 26 CHAIN 267 DISULFID 309 37 DISULFID 309 37 DISULFID 313 37	This SWISS-PROT ( between the Swis the European Bio use by non-proi modified and this entities require or send an email	GALLUS.  [1] [1] [1] [1] [1] [1] [1] [1] [1] [1	LT 1 CHICK STAN O42220; 15-JUL-1999 (Rel. 3 15-JUL-1999 (Rel. 3 16-OCT-2001 (Rel. 4 Growth/differentiat GDF8 OR MSTN. Gallus gallus (Chic Eukaryota: Metazoa; Archosauria; Aves;
EMBL; AF019621; AAB86688.1; HSSP; P18075; IBMP. InterPro; IFR001839; TGF-bet InterPro; IFR001839; TGF-bet InterPro; IFR001811; TGFb_N. Pfam; PF00019; TGF-beta; 1. Pfam; PF00068; TGFb_propepti ProDom; PD000357; TGF-beta; SMARR; SM00204; TGFB; 1. SMARR; SM002050; TGF_BETA_1 GROWTH factor; Cytokine; Gly GROWTH 22 GROWTH 37 GROWTH 26 GROWTH 26 GROWTH 37 GROW	This SWISS-PROT entry is copyright. It is prod between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt or send an email to license@isb-sib.ch).	OR OR OR OR	STAN Rel. 3 Rel. 4 entiat entiat (Chic tazoa;
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Homo sapiens (Human).
'``rvota; Metazoa; Chordata; (
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15-JUL-1999 (Rel. 38, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Growth/differentlation factor 8 precur
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                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SI SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: ACTS SPECIFICALLY AS MUSCLE GROWTH.
                                                                                                                                                                                                             pF00019; TGF-beta; 1.
pF00688; TGFb processing the process of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             le muscling in cattle due to mutations in the myostatin Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                                                                                                                    factor;
                                                                                                                                                         PS00250;
                                                                                                                                                                                                                                                                    IPR001839;
IPR001111;
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                                                                                                                                                                                                  TGFb_propeptide;
57; TGF-beta; 1.
                                                                                                                                  Cytokine;
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                                                                                                                                                         TGF_BETA_1; 1.
    266
375
340
372
374
                                                                                                                                                                                                                                                                                         TGF-beta.
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0; Mismatches
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a M., Nair G
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SIGNAL
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pronom: PD000357; TGF-beta; 1.
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MELGA
                                                                                                                                                                                                                                                                                                                                                                                                         "Double muscling in cattle due to me proc. Natl. Acad. Sci. U.S.A. 94:12 -i - EUNCTION: ACTS SPECIFICALLY AS
                                                                                                                                 SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1;
                                                                                                                                                                                                                            EMBL; AF019625; AAB86692.1; ALT_INIT HSSP; P18075; 1BMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
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Eukaryota; Metazoa; Chordata; Crani
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InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                  McPherron A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98024153; PubMed=9356471;
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                                                                                                                                                                                                                                                                                                                                                                                   MUSCLE GROWTH.
SUBUNIT: HOMODIMER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108;
                                                                                                                  factor;
                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
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                                                                                                       Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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99.1%;
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                                                                                                       Glycoprotein;
POTENTIAL.
 MW.
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                                                                                                                                                                                                                                                                                                                                                                      THE TGF-BETA FAMILY
                       POTENTIAL.

GROWTH/DIFFERENTIATION F

GROWTH/ALARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
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N-LINKED (GLCNAC.
D2AEAB732AEB4E77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (PO:
; EBFF6129725E6AFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           e to mutations in the 
94:12457-12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata;
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                                                                                                                    Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata;
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                         SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                             REGULATOR
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                                                                               FACTOR
             (POTENTIAL).
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the Euro
                     ProDom;
SMART; S
                                                                                                                                             EMBL;
                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                   EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
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Submitted (SEP-1998) to
-i- FUNCTION: ACTS SPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
MEDLINE=98024153; PubMed=9356471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, I
16-OCT-2001 (Rel. 40, I
Growth/differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-DUROC, HAMPSHIRE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McPherron A.C., Lee S.-J.;
"Double muscling in cattle due to mutations in the myostatin Proc. Natl. Acad. Sci. U.S.A. 94:12457;12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIG
                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-10 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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Voelker G.R., Conroy J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                   InterPro; IPR001839; InterPro; IPR001111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Porcine myostatin cDNA Yorkshire pigs.";
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                                                                                                                                        L; AF019623; AAB86690.1; -.
L; AF188635; AAF02770.1; -.
L; AF188636; AAF02771.1; -.
L; AF188637; AAF02772.1; -.
L; AF188638; AAF02773.1; -.
L; AF03355; AAF02773.1; -.
L; AF03355; AAF02783.1; -.
L; AF033798; AAC62489.1; -.
P; P18075; 18MP.
                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Event Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY). SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUSCLE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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AF188635;
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AF188638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00019; TGF-beta; 1. pF00688; TGFb_propeptide; m; PD000357; TGF-beta; 1.
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E; PS00250;
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                     TGFB;
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SPECIFICALLY AS A NEGATIVE
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                                                                                                                                                                                                                                                                                                                                                                                         rmatics Institute. There are no resi
                                                                                                      TGFb_N.
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                                                                                                                         TGF-beta.
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Duroc,
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InterPro; IPR001839; TGF-bet InterPro; IPR001111; TGFb\_N.

PF00019;

TGF-beta; TGFb\_propeptide;

MGD; MGI:95691; Gdt

Gdf8.

U84005; AAC53167.1; P18075; IBMP.

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                                                                                                                                                                                                                                                                                          McPherron A.C., Lawler A.M., Lee S. T., McPherron A.G., Lawler A.M., Lee S. T., McPherron of skeletal muscle mass in mice by a new TGF-be superfamily member.";
Nature 387:83-90(1997),
Nature 387:83-90(1997),
Nature 387:83-90(1997)
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _MOUSE
                                                                                                                                   This SWISS-PROT entry is copyright. It is produced th between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDF8 OR MSTN.
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             008689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDF8_MOUSE
                                                                                                                                                                                                                                                                                                                                               MEDLINE=97284412; PubMed=9139826; McPherron A.C., Lawler A.M., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CD-1; TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                       SKELETAL MUSCLE. WEAK EXPRESSION IN ADIPOSE TISSUE.

DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-COITUM IN

ONE-THIRD OF DEVELOPING SOMITES. AT DAY 10.5, EXPRESSED IN THE

MYOTOME COMPARTMENT OF SOMITES. AT LATER STAGES OF DEVELOPMENT,

DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION
                                                                                                                                                                                                                                                               SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING
                                                                                                                                                                                 CONTINUES IN ADULTHOOD. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s
                                                                                                                                                                                                                                                                                        MUSCLE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tactor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel.
(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              35, Created)
35, Last sequence update)
40, Last annotation update)
ation factor 8 precursor (GDF-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
266
375
340
372
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374
339
                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                    Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.0%;
99.1%;
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.
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GROWT/DIFFERENTIATION FACTOR
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 622; DB 1
Pred. No. 4e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (PC
                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0F658685EFDA3418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                          It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal
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                                                                                                                                               and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Myostatin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                     TGF-beta
                                                                                                                                    he EMBL outstation restrictions on it
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                                                                                                                                                                                                                                                                                                    SKELETAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Sin
Matches 108;
InterPro, IPR001111, InterPro, IPR001111, InterPro, IPR001111, InterPro, IPR00019; TGF-beta; 1.

Pfam; PF00688; TGFb_propeptide; 1.

ProDom; PD000357; TGF-beta; 1.

R PROSITE; PS00250; TGFB; 1.

R PROSITE; PS00250; TGFB; 1.

PROSITE; PS00250; TGFB; 1.

POTENTIAL.

POTENTIAL.
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DISULFID
CARBOHYD
SEQUENCE
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035312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROPEP
CHAIN
                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McPherron A.C., Lee S.-J.;

"Double muscling in cattle due to mutations in the myostatin Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).

-I- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SHOUSCLE GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth/differentiation GDF8 OR MSTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Growth factor;
SIGNAL
                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98024153; PubMed-9356471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L5-JUL-1999 (Rel. 38, Created)
L5-JUL-1999 (Rel. 38, Last sequence up
L6-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                         P18075;
                                                                                                                                                                                                                                                            AF019624; AAB86691.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00204; T
E; PS00250;
                                                                                                                                                                         IPR001839; TGF-beta.
IPR001111; TGFb_N.
IPR001111; TGF-b_N.
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50; TGF_BETA_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
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99
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POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 622; DB Pred. No. 4e-6 0; Mismatches
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GROWTH/DIFFERENTIATION F
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
THE POSITION OF THE POSITION 
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N-LINKED (GLCNAC. . .) (POT
; 3E19814DD62C08BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tation update)
precursor (GDF-8) (Myostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     622; DB 1
No. 4e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376
                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal
                                                                                                                                                                                                                                                                                                                                                            There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                       Usage
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RESULT 7
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Best Local S
Matches 108
                                                                                                                          PROSITE; Pactor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
DISULFID
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DISULFID
CARBOHYD
SEQUENCE
    Growth fa
SIGNAL
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Growth/differentiation factor 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       018828;
                                                                                                                                                                                Pfam; PF00019; TGF-beta; I.
pfam; PF00068; TGFb_propeptide;
ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
MEDLINE-98024153; Pubme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDF8 OR MSTN.
                                                                                                                                                                                                                                                                                                           EMBL; AF019619; AAB86686.1; -. HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Papio hamadryas (Hamadryas baboon)
                                                                                                                                                                                                                                                                    InterPro; IPR001839; TGF-beta
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McPherron A.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecinae; Papio
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L5-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY). SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uble muscling in cattle due to mutations in the c. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997). FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUSCLE GROWTH
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                                                                                                                                                                PS00250; TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 38, Created)
(Rel. 38, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                           Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee
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99.1%;
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POTENTIAL
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GROWTH/DIFFERENTIATION F
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Pred. No. '
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N-LINKED (GLCNAC. . .) (PO
; 933043D8C8C3294B CRC64;
                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursor (GDF-8) (Myostatin).
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                                                                                                                                           Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Eutele
i; Cercopithecidae;
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Best Local :
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              CARBOHYD
CARBOHYD
                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                             Proc.
                                                                                                      SIGNAL
                                                                                                                                     Pfam; PF00688; TGFb_propeptide; ProDom; PD000357; TGF-beta; 1. SMART; SM00204; TGFB; 1.
                                                                                                                                                                       InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHEEP
                                                                                                                  Growth
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98024153; PubMed=9356471; McPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDF8 OR MSTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Growth/differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          018830;
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                                                                                           PROPEP
                                                                                                                            PROSITE; PS00250;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         "Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY). SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                uble muscling in cattle due to mutations in the myostatin c. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997). FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SI
                                                                                                                                                                                                                                                                                                                                                         MUSCLE GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                         AF019622; AA
P12643; 3BMP
                                                                                                                  factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                               Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                    AAB86689.1;
                                                                                                                                                                                                                                                                                                                                                                                                                          muscle;
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40,
                                                                                                                           TGF_BETA_1;
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98.2%;
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Last annotation update;
n factor 8 precursor (GDF-8) (Myostatin).
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                                                                                                               Glycoprotein; Signal
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GROWTH/DIFFERENTIATION FACTOR 8
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OF THE STANDARD (GLCNAC...) (POTENTIANED (GLCNAC...) (POTENTIANED (GLCNAC...) (POTENTIANED (GLCNAC...)
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Pred. No. 1.9e-62;
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                                                                                                      POTENTIAL.
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              (POTENTIAL).
                        (POTENTIAL).
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Best Local
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                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDF8_BOVIN STANDARD; PRT; 375 AA. 018836; 018829; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Growth/differentiation factor 8 precursor (GDF8 OR MSTN_OR MH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOVIN
                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Double muscling in cattle due to mutations in the myostatin Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98024153; PubMed=9356471; McPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANTS STRAIN-HOLSTEIN; TISSUE-Skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piedmontese cattle.";
Genome Res. 7:910-916(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANT M. STRAIN-FRIESIAN; TISSUE-Muscle, aumenLine-97458167; PubMed-9314496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
Bovidae; Bovinae; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kambadur R., Sharma M., Smith T.P
"Mutations in myostatin (GDF8) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUSCLE GROWTH.
SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING
SKELETAL MUSCLE. HIGHEST LEVELS FOUND IN THE HINDLIMB MUS
M.SEMIMEMBRANOSUS AND M.BICEPS FEMORIS; LOW LEVELS IN OTH
                                                                                                                                                                                                                                                                                                                                                                                           LOW LEVELS ARE FOUND UP TO DAY 29 EMBRYOS. LEVELS INCREASE FI DAY 31 UP UNTIL LATE GESTATION.

DISEASE: DEFECTS IN GDF8 ARE THE CAUSE OF THE DOUBLE-MUSCLE PHENOTYPE OR MUSCULAR HYPERTROPHY (MH), AN AUTOSOMAL RECESSIV DISEASE FREQUENTLY FOUND IN THE BELGIAN BLUE AND PIEDMONTESE CATTLE BREEDS. THIS DISEASE IS CHARACTERIZED BY AN INCREASED NUMBER OF MUSCULE FIBERS (HYPERPLASIA), RESULTING IN AN INCREMUNDED OF THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE: WIDELY
                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                              MUSCLE MASS OF 20-25%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HINDLIMB MUSCLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFLFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHQANPKGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPGMVVDRCGCS
                                                                                              AF019761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105;
                                               P18075;
                                                                    AF019620;
                                                                                                                                             s requires a license agreement (See http://www.an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                               1BMP.
                                                                    AAB81508.1; -.
AAB86687.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 612; DB
Pred. No. 5.5e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.L., Bass J.J.;
in double-muscled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXPRESSED THROUGHOUT DEVELOPMENT DAY 29 EMBRYOS. LEVELS INCREASE FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MH TYR-313. and Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MH LEU-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5e-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GDF-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYR-313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Belgian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Myostatin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                       .isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                   INCREASED

AN INCREASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PING AND AB MUSCLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECESSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADULT
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InterPro;

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  RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 106; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBFH MOUSE

09Z1W4; 09QX55; 09R221;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1)
SEQUENCE FROM N.A.
MEDLINE-99177155; PubMed-10075854;
Wolfman N.M., Celeste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000357; TGF
SMART; SM00204; TGFB;
PROSITE; PS00250; TGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
Pfam;
                      "Expression of growth/differentiation factor 11, Expression of growth/differentiation factor 11, BM2/TGFbeta superfamily during mouse embryogenes Mech. Dev. 80:185-189(1999).
                                                                                                                                                                                                                                                                       MEDLINE=99318097; PubMed=10391213;
McPherron A.C., Lawler A.M., Lee S.-J.;
"Regulation of anterior/posterior patterning
growth/differentiation factor 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth factor; SIGNAL
                                                                                                                                                          SEQUENCE OF 75-405 FROM N.A. MEDLINE-99173787; PubMed-10072786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-129/SVJ
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00019; TGF-beta; 1. PF00688; TGFb_propept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       potent mesoderm indu
1. 208:222-232(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BMP expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGFb_propeptide;
57; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA,
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375
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Rodentia;
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97.2%;
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SIGNAL THAT ACTS GI
ANTERIOR/POSTERIOR
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inducer in l
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

BY SIMILARITY.

INTERCHAIN (BY SIMILARITY).

INTERCHAI
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                             mouse embryogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E1B791AD92D4A9E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                611;
No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse limb,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hattersley
                            GLOBALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
.1e-62;
AXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              limb, spinal
embryos.";
                                                                                                                                                                                                                                                                                                      of
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DURING DEVELOPMENT.
                                                                                                                                                                                                                                                                                                      the axial skeleton
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                                                                                                         Ø
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                                                                                   new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G., Hewick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
;; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                            member
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cord,
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RESULT 11
GDFB\_HUMAN
ID GDFB\_H
AC 095390

GDFB\_HUMAN O95390; Q9UID1;

STANDARD; ; Q9UID2;

PRT;

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                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF100906; AAC72853.1; -.
EMBL; AF100904; AAC72853.1; JOI
EMBL; AF100905; AAC72853.1; JOI
EMBL; AF028337; AAF21633.1; -.
EMBL; AF028335; AAF21633.1; JOI
EMBL; AF028336; AAF21633.1; JOI
EMBL; AF028336; AAF21633.1; JOI
EMBL; AF092734; AAF21633.1; JOI
EMBL; AF092734; AAD05267.1; -.
HSSP; P18075; 1BMP.
MGD; MGI:1338027; Gdf11.
InterPro; IPR001839; TGF-beta.
InterPro; IPR001811; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth
SIGNAL
PROPEP
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pfam; pF00019; TGF-beta; 1.
pfam; pF00688; TGFb_propeptide;
proDom; pD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
pROSITE: pS00250; TGF_BETA_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                SEQUENCE
357
                                                                                                 297
                                               61
                                                                                                                                                    H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: FIRST STRONGLY EXPRESSED IN RESTRICTED DOMAINS AT 8.5 DAYS POST COLTUS (DPC) WHERE IT IS HIGHEST IN THE TAIL BUD. AT 10.5 DPC, EXPRESSED IN THE BRANCHIAL ARCHES, LIMB BUD, TAIL BUD AND POSTERIOR DORSAL NEURAL TUBE. LATER, EXPRESSED IN TERMINALLY-DIFFERENTIATED ODONTOBLASTS, THE NASAL EPITHELIUM, RETINA AND SPECIFIC REGIONS OF THE BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
SUBUNIT: HOMODIMER: DISCULFIDE-LINKED (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted (Probable).
SUBCELLULAR LOCATION: SECRETED IN THE DEVELOPING LIMB B TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB B INITIALLY DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALITO REGIONS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE TGF-BETA, FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DENTAL PULP AND BRAIN.
                       VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                            DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
: |||||||:||:||:||:|||||||||
VQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPGMVVDRCGCS
                                                                                                 NLGLDCDEHSSESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHL
                                                                                                                                                                                                      97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor;
                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine;
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405
213
213
370
402
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171
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89
                                                                                                                                                                                                                           . 48;
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POTENTIAL
                                                                                                                                                                                                                                                                                                                                   MW.
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JOINED
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY GLONG.
N-LINKED (GLONG.
E-> G (IN REF. 3
E-> G (IN REF. 3
                                                                                                                                                                                                   Score 574; DE Pred. No. 1.2e 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
GROWTH/DIFFERENTIATION FACTOR
                                                                                                                                                                                                                                                                                                                             -> G (IN REF. 3).
-> N (IN REF. 2).
A74E382710A14781
                                                                                                                                                                                                                           574;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions on 11 ng as its content is in ~~ ved. Usano '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
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..2e-57;
les 5;
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                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                 Length 405;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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L ARCHES, LIMB
LATER, EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIMB BUD,
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16-OCT-2001
16-OCT-2001
                                                             CARBOHYD
SEQUENCE
                                                                                                                                                                                                                               pfam; PF00019; TGF-beta; 1.
pfam; PF00688; TGFb_propeptide;
ProDom; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                     EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formations are removed.
                                                                                                                                                            CHAIN
                                                                                                                                                                                   Growth factor; SIGNAL
                                                                                                                                                                                                                                                                                               MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McPherron A.C., Lawler A.M., Lee S.-J.; "Regulation of anterior/posterior patterning growth/differentiation factor 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A novel BMP expressed in developing mouse limb, bud is a potent mesoderm inducer in Xenopus embr Dev. Biol. 208:222-232(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Fetal brain;
MEDLINE=99177155; PubMed=10075854;
Gamer L.W., Wolfman N.M., Celeste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human Eukaryota; Metazoa;
                                                                                                                                    DOMAIN
                                                                                                                                                 DOMAIN
                                                                                                                                                                         PROPEP
                                                                                                                                                                                                            PROSITE; PS00250;
                                                                                                                                                                                                                      SMART; SM00204; TGFB;
                                                                                                                                                                                                                                                                     InterPro; IPR001839;
InterPro; IPR001111;
                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
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             y Match
Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT. PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                               603936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genet. 22:260-264(1999)
                                                                                                                                                                                                                                                                                                                     AF100907; AAC72852.1; -. AF028333; AAF21630.1; -. AF028334; AAF21631.1; -.
                                                                                                                                                                                                                                                                                                        P18075; 1BMP
   97; Conserv
                                                                                                                                                                                                                                                                                                                                                                  email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (Human).
3 (Human).
Chordata; (
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(Rel.
(Rel.
   Conservative
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299
210
210
313
341
341
371
                                                                                                                                                                                              Cytokine;
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                                                                                                                                                                                                            TGF_BETA_1;
                                                                         298
407
41
215
372
404
406
371
94
                                                                                                                                                                                                                                                                     TGF-beta.
TGFb_N.
             91.4%;
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Last annotation
n factor 11 precu
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                                                                                                                                                                                              Glycoprotein; Signal.
                                                             W.
                                                                    BY SIMILARITY.

GROWTH/DIFFERENTIATION FACTOR 11.

POLY-ALA.

POLY-GLY.

BY SIMILARITY.

LINERD (GLCNAC...) (POTENTIAL).
 Score 574; DB
Pred. No. 1.2e
7; Mismatches
  7;
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                                                             E8FF48E363635BA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor (Bone morphogenetic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus embryos
                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
DB 1; 1
..2e-57;
les 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hattersley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the axial skeleton
                       Length 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spinal
  Indels
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                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                 he EMBL outstation restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hewick R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cord,
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                                                                                                                                                                                                                                                                                                                                                                                                                                collaboration
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 Gaps
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DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL

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                                          Query Match
Best Local S
Matches 95
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                                                                                                                                                                    CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Zebra dar Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                InterPro: IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
ProDom; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                          ZFIN;
                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collal between the Swiss Institute of Bioinformatics and the EMBL outsi the European Bioinformatics Institute. There are no restrictions
                                                                                                   SEQUENCE
                                                                                                              CARBOHYD
                                                                                                                        CARBOHYD
                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                  Growth
                                                                                                                                                                                                                                         SMART; SM00204;
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                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Skeletal muscle; MEDLINE=98024153; PubMed=9356471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDF8 OR MSTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Growth/differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000
30-MAY-2000
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O42222;
                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McPherron A.C., Lee S.-J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUSCLE GROWTH
          DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEEVFLQKYPHTHL
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                                                                                                                                                                                                                                                                                                           ZDB-GENE-990415-165;
                                                                                                                                                                                                                                                                                                                     AF019626; AAB86693.1; P12643; 3BMP.
                                          ch 89.6%;
l Similarity 87.2%;
95; Conservative
                                                                                                                                                                                                                             PS00250; TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 41, Last annotation update)
erentiation factor 8 precursor (GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMODIMER;
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                                                                                                                                                                                                                                      TGFB;
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265
374
339
371
373
373
                                                                                                   42060
                                                                                                                                                                                                                 ine;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFIDE-LINKED (BY SIMILARITY).
TO THE TGF-BETA FAMILY.
                                                                                                                                                                                         Glycoprotein;
POTENTIAL.
POTENTIAL.
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                                                                                               GROWTH/DIFFERENTIATION FACTOR 8
BY SIMILARITY.
BY SIMILARITY:
BY SIMILARITY:
BY SIMILARITY:
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . . ) (POTENTI
                                                                                                                                                                                                                                                                                                          gdf8.
                                          Score 563; DB
Pred. No. 1.9e
ll; Mismatches
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ca; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374
                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib
                                                                                                                                                                                                                Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostei;
                                          DB 1; 1
l.9e-56;
nes 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GDF-8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGULATOR OF
                                                               Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Myostatin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myostatin
                                                                                                              (POTENTIAL)
                                                                                                                        (POTENTIAL)
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                                                                  Matches
                                                                            Query Match
Best Local
                                                                                                                     DOMAIN
DISULFID
DISULFID
CARBOHYD
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Dental pulp;

MEDLINE-99173787; PubMed-10072786;

Nakashima M., Toyono T., Akamine A., Joyner A.;

"Expression of growth/differentiation factor 11, a

BMP/TGFbeta superfamily during mouse embryogenesis.

Mech. Dev. 80:185-189(1999).
                                                                                                                                                                                                                                                   Pfam; PF00019; TGF-beta; 1. Pfam; PF00688; TGFb_propeptide; ProDom; PD000357; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09Z217;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                       Growth
                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                           SMART; SM00204; TGFB;
                                                                                                                                                                                                                                                                                                           EMBL; AF092733; AAD05266.1; HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDF11 OR BMP11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Growth/differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDFB_RAT
                                                                                                                                                                                                  PROPER
                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                     InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6-OCT-2001 (Rel. 6-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326
                      243
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                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                            <u>--</u>
                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITION.
IDENTITY ALONG THE ANTERIOR, POSTERIOR AXIS DURING DEVELOPMENT.
PLAY CRITICAL ROLES IN PATTERNING BOTH MESCODERMAL AND NEURAL
TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN (BY SIMILARITY).
SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted (Probable).
SUBCELLULAR EDCATION: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVV
                     NLGLDCDEHSSESRCCRYPLTVDFEASGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHL
                                  DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                       factor;
                                                                                                                                                                                                                                 PS00250;
                                                                                                                      345
                                                                                                                                243
154
257
315
345
                                                                Conservative
                                                                                                                       AΑ;
                                                                                                                                                                                                                     Cytokine; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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. 40, Last sequ.
. 40, Last anno
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>345
159
316
315
345
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Last annotation update)
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                                                                                                                      MW.
                                                                        Score
Pred.
                                                                                                                                        GROWTH/DIFFERENTIATION FACTOR 11.
POLLY-GLY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL
                                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 precursor (Bone morphogenetic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sciurognathi;
                                                                                                                      81D5B93FED6B0443 CRC64;
                                                                Mismatches
                                                                          527;
No. 2
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                                                                          DB 1;
.1e-52;
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 103
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                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                    restrictions on
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                                                              Gaps
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NON_TER
         PROSITE; PS00250; 105_____.

Growth factor; Hormone; Glycoprotein.
                                                                                               HSSP;
                                                                                                        EMBL; X83376; CAA582
EMBL; X69620; CAA493;
PIR; S31441; S31441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glandular organs of the mous Mech. Dev. 50:229-245(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CBA X NMR1; TISSUE=Testis; MEDLINE=95344997; PubMed=7619733;
                                          ProDom; PD000357; TGF-beta; 1. SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Albano P.M., Groome N., Smith J.C. "Activins are expressed in preimpl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gilbert S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                               Pfam; PF00019; TGF-beta;
                                                                                      MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    and EC cells and are regulated on their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93321614; PubMed=8330535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 134-255 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Activin disrupts epithelial branching glandular organs of the mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ritvos O., Tuuri T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-234 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                          nterPro; IPR001839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303
                                                                                                                                                                                                                                                                                                                                           ACTIVINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPGMVV
                                                                                    MGI:96571;
                                                                                               P12643; 3BMP
                                                                                                                     CAA58290.1;
CAA49326.1;
                                                                                     Inhbb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eramaa M.,
                                                                          TGF-beta
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Development 177:711-723(1993).

-!- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,

-!- FUNCTION: THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND
INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION.
                                                                                                                                                                                                                                                                                                                                         SUBUNIT: DIMERIC, LINKED BY ONE OR MORE INHIBIN A IS A DIMER OF ALPHA AND BETA-B.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
ACTIVIN A IS A HOMODIMER OF BETA-B.
ACTIVIN B IS A HOMODIMER OF BETA-B.
                                                                                                                                                                                                                             TISSUE SPECIFICITY: UTERUS, TESTIS, OVARY, LUNG. CJ7 EMBRYONIC STEM CELLS, AND POSSIBLY IN LIVER. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
                                                                                                                                                                                                                                                                                                               ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT COMPOSITION. INHIBINS APPEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preimplantation mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K., Hilden K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ТО
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFIDE
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                                                                                                                                                                                                                                                                                          LUNG,
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                                                                                                                                                                                                                                                                                       KIDNEY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTIONS
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                                                                                                                                              collaboration -
                                                                                                                                                                                                                                                                                          BRAIN,
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PRESULP PROBLEM PROBLE
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DISULFID
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                         This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94009920; PubMed=8405668;
Helde K.A., Grunwald D.J.;
"The DVR-1 (V91) transcript of zebrafish is maternally supplied and distributed throughout the embryo.";
Dev. Biol. 159:418-426(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi
Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVR1_BRARE STANDARD; PRT; 3
P35621;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dev.
                                                                                                                                                                                    use by non-profit institutions as low-modified and this statement is not removementitles requires a license agreement (so or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVR-1 protein precursor. VG1 OR DVR1 OR DVR-1.
                                                                                          EMBL; U00931; AAC27347.1;
HSSP; P12643; 3BMP.
ZFIN; ZDB-GENE-980526-389;
                                                                                                                                                                                                                                                                                the
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                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITI: NOVELLE BLASTOMERES.

DISTRIBUTED AMONG ALL BLASTOMERES.

DEVELOPMENTAL STAGE: CONCENTRATED IN THE STREAMING CYTOPLASM IN

DEVELOPMENTAL STAGE: CONCENTRATED IN THE STREAMING CLEAVAGE AMONG ALL

JUST-FERTILIZED EGGS. EVENLY PARTITIONED DURING CLEAVAGE, BLASTULA AND

BLASTOMERES. ABSENT IN THE YOLK CELL DURING CLEVAGE, BLASTULA AND

BLASTOMERES. ABSENT IN THE YOLK CELL DURING CLEVAGE, BLASTULA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT. SUBUNIT: HOMODIMER (PROBABLE).
TISSUE SPECIFICITY: ABUNDANT IN OVARIES AND EG
                                                                                                                                                                                                                                                                                European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF MESODERM OR ENDODERM EITHER AS A COFACTOR IN AN INSTRU
                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                        GASTRULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -HTHLVHQANPRG-SAGP---CCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
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                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
50; Conserv
                                           IPR002400;
IPR001839;
                        IPR002400; GF_cysknot.
IPR001839; TGF-beta.
IPR0011111; TGFb_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
                                                                                            dvr1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Mismatches
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BY SIMILARITY.
BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
H -> D (IN REF. 2).
M; 2524B21DC648D9A9 CRC64;
                                                                                                                                                                                                                                    is not removed.
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Pred.
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No. 4e-20;
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                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
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PF00019;

TGF-beta;

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PROSITE; PS00250; TGF_BETA_1; 1.
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                                                                                                                                                                                                                              Growth factor;
                                                                                                                                                                                                    CHAIN
                                     249
                  63
                                                      11 TESRCCR-YPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYPHTH-----LVH 62
            QANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGC
                                   SFDPKGTPQPCCVPIKLSPISMLYYDNNDNVVLRHYEDMVVDECGC
                                                                         Similarity 43.446; Conservative
                                                                                                                      296
355
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254
283
287
287
319
108
179
                                                                                                                         AA;
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355
320
352
354
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108
179
                                                                                                                         40201 MW;
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                                                                         Score 239; DB Pred. No. 9.5e 6; Mismatches
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY)
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                                                                                                                         OED5B9850EBFB222 CRC64;
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9.5e-20;
36;
                                                                                           Length 355
                                                                          Indels
                  108
354
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                                                                        Gaps
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 $_{\cdot}^{\omega}$ 

Search completed: Job time: 215 sec May 20, 2002, 09:24:50

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2002, 09:20:50; Search time 24.89 Seconds (without alignments) 757.591 Million cell updates/sec

Title: Perfect score: US-09-754-826-2 628

Sequence: 1 DFGLDCDEHSTESRCCRYPL.....KEQIIYGKIPAMVVDRCGCS 109

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

562222 seqs, 172994929 residues

earched:

Total number of hits satisfying chosen parameters:

562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL\_19:\*
1: sp\_archea:\*
2: sp\_bacteria
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_inverteb:
6: sp\_mammal:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*

sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\* sp\_organelle:\*

sp\_phage:\* sp\_rodent:\*
sp\_virus:\* sp\_plant:\*

sp\_vertebrate:\*
sp\_unclassified:\*
sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

16	15	14	13	12	11	10	9	8	7	0	5	4	ω	2	1	Result No.
556	557	557	557	557	557	557	560	563	592	599	611	617	622	622	622	Score
88.5	88.7	88.7	88.7	88.7	88.7	88.7	89.2	89.6	94.3	95.4	97.3	98.2	99.0	99.0	99.0	Query Match
373	376	376	376	373	373	373	385	389	185	185	375	375	375	375	162	Length
13	13	13	13	13	13	13	13	13	6	σ	6	13	σ	6	σ	DB
Q90W17	Q90WC8	Q90WC9	Q98TB4	Q90ZD1	Q90ZD2	Q9DDI8	Q90W05	090440	Q9MZ18	Q95N11	Q95N97	Q98SP0	Q95J86	Q9GM97	Q9TSY2	ID
	Q90wc8 morone amer	Q90wc9 morone saxa	Q98tb4 oreochromis	Q90zdl oncorhynchu	Q90zd2 oncorhynchu	Q9ddi8 salmo salar	Q90w05 sparus aura	Q90yy0 ictalurus p	Q9mz18 ovis aries	Q95nll capra hircu	Q95n97 bos taurus	Q98sp0 gallus gall	Q95j86 macaca fasc	Q9gm97 equus cabal	Q9tsy2 sus scrofa	Description

Query Match Best Local Similarity Matches 108; Conserv

Conservative

99.0%;

Score 622; DB 6; Length 162; Pred. No. 4.1e-67; 0; Mismatches 1; Indels

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Gaps

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45	44	43	42	41	40	39	38	37	36	3 5	34	3 3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
15.	215.5	16	222	222		223.5		•				•	•		234.5	238	247	286	294.5	94	302	311	394	522	547	550	552	555
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447	294	399	373	373	411	361	349	354	138	115	115	115	392	393	115	395	370	58	598	598	104	191	78	107	96	373	377	376
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		xenopu		Q90723 gallus gall	Q9u418 branchiosto	096504 branchiosto	097138 brugia mala		23			Q9dgfl cyprinus ca		Q90261 brachydanio		Q9pwg6 anguilla ja	Q91350 xenopus lae	Q95mf3 sus scrofa	drosophi	rosophila	Q90z79 ictalurus p		Q9xs86 equus cabal	S	Q9w759 cairina mos	salvel	3 morone o	Q90w06 umbrina cir

### ALIGNMENTS

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SEQUENCE FROM N.A.  MEDLINE=20078370; PubMed=10612246;  Stratil A., Kopecny M.;  "Genomic organization, sequence and polymorphism of the porcine myostatin (GDF8; MSTN) gene.";  Anim. Genet. 30:468-470(1999)!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  EMBL; AJ237920; CAB408444.1;  HSSP; P18075; 1BMP. InterPro; IPR002400; GF_cysknot. InterPro; IPR002400; GF_cysknot. FinterPro; IPR001839; TGF-beta. Pfam; PFR00438; GFCYSKNOT. PRODOM; PFR00438; GFCYSKNOT. PRODOM; PD000357; TGF-beta; 1. SMART; SM00204; TGFB; 1. PROSITE; PS00250; TGF_BETA; 1. Glycoprotein.  1 1 SEQUENCE 162 AA; 18290 MW; FE353334512856E CRC64;	O9TSY2 PRELIMINARY; PRT; 162 AA. Q9TSY2; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) MYOSTATIN (FRAGMENT). MSTN. Sus scrofa (Pig). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. NCBI_TaxID-9823; [1] SEOTORNCE EROM N A	JLT 1 SY2

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01-MAR-2001
01-DEC-2001
                                              Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
Cercopithecinae; Macaca.
VCBI_TaxID=9541;
                                                                                                                                                                                             Q95J86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular cloning of equine myostatin cDNA and serum le myostatin in horse.";

Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

EMBL, AB033541; BAB160461; -.

HSSP; P18075; 1BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Equus caballus (Hórse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
SEQUENCE FROM N.A.
TISSUE-GASTROCNEMIUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein
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InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
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                                                                                                                 Macaca
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108; Conserv
                                                                                               fascicularis (Crab eating macaque) (Cynomolgus monkey).
pta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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l (TrEMBLrel.
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Pred. No. 1e-66;
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                                                                                Cercopithecidae;
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01-JUN-2001
01-JUN-2001
01-DEC-2001
    Q95N97
                                                                                                                                                                                                                                                                                        Glycoprotein.
SEQUENCE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO 'EMBL; AF346599; AAK18000.1; HSSP; P18075; 1BMP
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107; Conservative
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98.2%;
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InterPro; IPR002048; EF-hand.
InterPro; IPR001839; TGF-beta.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00088; TGFb_propeptide; I
ProDom; PD000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smock S.L., Owen T.A.;
"Cloning of the open reading frame DNA for mac (cynomolgus macaque) myostatin (GDF8).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ EMBL; AY055750; AAL17640.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           development."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                            PROSITE; PS00018; EF_HAND; UNKNOWN_1.
PROSITE; PS00250; TGF_BETA; 1.
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VHQANPRGPAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                     DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 AA; 42722 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                               42717 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression of the chicken GDF-8 during
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                                                                                                                                       Score 617; DB Pred. No. 4e-6 0; Mismatches
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Last sequence update)
Last annotation updat
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0; Mismatches
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                                                                                                                                                                                                                               D980E286426E4D4F CRC64;
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                                                                                                                                                        8 617; DB 13
No. 4e-66;
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No. le-66;
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01-DEC-2001
01-DEC-2001
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                                                                                                                                                     Lian Z., Pan Q., Chen H., Ji "Cloning of intron 2 of the Submitted (APR-2001) to the EMBL; AY032689; AAK49790.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-21343337; PubMed-11451380;

Jeanplong F., Sharma M., Somers W.G., Bass J.,

"Genomic organization and neonatal expression"
                                                                                                                                                                                                            Bovidae; Caprinae;
NCBI_TaxID=9925;
                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                   Capra hircus (Goat)
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Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
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VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS
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VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCG
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AF320998; AAG48116.1; -.
NCE 375 AA; 42551 MW; 84E1A
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185 /
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l (TrEMBLrel.
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42551 MW; 84E1AB20650C05F6
                                                                                     95.4%;
96.3%;
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97.2%;
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19,
                                                                                                                           MW;
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myostatin gene in
EMBL/GenBank/DDBJ
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Pred.
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Pred. No. 2.8e-64;
2; Mismatches 2
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ion of
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the bovine
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RESULT
Q9MZ18
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01-OCT-2000
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01-DEC-2001
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NON_TER
SEQUENCE
                                                                                      SEQUENCE FROM N.A.

KOCADAS A.M., Liu Z.J.;

KOCADAS A.M., Liu Z.J.;

MOLECULAR Characterization and expression of channel catfish (Ictalurus punctatus).";

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; AF396747; AAK84666.1; -.

SEQUENCE 389 AA; 43600 MW; 569FB952B7E9E17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lian 2., Jin H., Li N.;
"Cloning of intron 2 of the myostatin gene in submitted (MAY-2000) to the EMBL/GenBank/DDBJ"-!-SIMILARTY: BELONGS TO THE TGF-BETA FAMILY EMBL; AF266758; AAF78069.1; --
HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                          Actinopterygii; Neopterygii; Siluriformes; Ictaluridae; Ic NCBI_TaxID=7998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Caprinae;
                                                                                                                                                                                                                                                                                                 Ictalurus punctatus (Channel
Eukaryota; Metazoa; Chordata;
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pfam; pF00019; TGF-beta; 1.
proDom; pB000357; TGF-beta; 1.
SMART; SM00204; TGFB; 1.
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185 AA;
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; Cetartiodactyla; Ruminantia; Pec
Ovis.
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15,
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                                                                                                                                                                                                                                                              i; Teleostei;
Ictalurus.
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Pred. No. 1.
2; Mismatche
Score 563; DB Pred. No. 1.3e B; Mismatches
                                                                                                                                                                                                                                                                                                 catfish).
; Craniata;
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Last sequence up
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                                       389;
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Conservative

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RESULT
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Matches
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Q1-MAR-2001 (TrEMBLrel. 1
Q1-OCT-2001 (TrEMBLrel. 1
Q1-DEC-2001 (TrEMBLrel. 1
MYOSTATIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygil; Neopterygil; Teleostel; Euteleostel; Neoteleostel; Acanthomorpha; Acanthopterygil; Percomorpha; Perciformes; Percoide; Sparidae; Sparus.
NCBL_TaxID-8175;
                                                                 SEQUENCE FROM N.A.

Ostbye T.K., Galloway T.F., Nielsen C., Gabo

"The two myostatin genes of Atlantic salmon

expressed in a variety of tissues.";

Submitted (DEC-2000) to the EMBL/GenBank/DDI
                                                                                                                                                           Salmo salar (Atlantic salmon).

Salmo salar (Atlantic salmon).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;

Perotacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of the myostatin gene in the gilthead seabream, Sparus aurata: sequence, genomic structure, and expression patter Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF258448; AAK53545.1; -
EMBL; AF258447; AAK53544.1; -
EMBL; AF258447; AAK53544.1; -
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                          Rescan P.-Y., Jutel I., Ralliere C.;
"Two myostatin genes are differentially
of the trout (Oncorhynchus mykiss).";
J. Exp. Biol. 0:0-0(2001).
EMBL; AF273035; AAK71707.1; -.
SEQUENCE 373 AA; 42049 MW; 9DD4771B
                                                                                                                                                                                                                                                                                                                                              Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Actinopterygii; Neopterygii; Teleostai; Euteleostai; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorl NCBI_TaxID-8022;
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InterPro; IPR001111; TGFb_N.
Pfam; PF00688; TGFb_propeptide;
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA; 1.
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; AJ297267; CAC19541.2;
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EMBL; AJ316006; CAC59700.1;
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HSSP; P12643; 3BMP.
  Q90ZD1
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Pred. No. 6.7e-59;
7; Mismatches 6
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01-DEC-2001
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; 
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroide 
Cichildae; Oreochromis.
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                                                                                                                                                                Glycoprotein.
SEQUENCE 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21150052; PubMed=11250920;
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BL, AF273036; AAK71708 1; -
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     characterization of two additional cDNA clones from worm and Morone americana.":
                                                                                                                                                                                                                                                                                                                                                                                                                  and Morone americana.",
Comp. Biochem. Physiol. B, Biochem. Mol.
EMBL; AF299910; AAK67983.1; -.
SEQUENCE 376 AA; 42794 MW; E2C5D61FF2
                                                                                                                  Morone americana (White perch).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopteryqii; Meopteryqii; Teleostei;
Acanthomorpha; Acanthopterygii; Percomor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Verto
Actinopterygii; Neopterygii; Teleostei; Eute
Acanthomorpha; Acanthopterygii; Percomorpha;
                                                               SEQUENCE FROM N.A.
TISSUE=SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence conservation among fish myostatin orthologues characterization of two additional cDNA clones from Moro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21292690; PubMed=11399495; Rodgers B.D., Weber G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-SKELETAL MU
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                                                   MEDLINE=21292690; PubMed=11399495;
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Physiol.
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i; Percomorpha; Perciformes;
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Mol.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein - protein search, using sw model

Run on: мау 20, 2002, 09:20:25; Search time 16.7 Seconds (without alignments) 627.170 Million cell updates/sec

....KEQIIYGKIPAMVVDRCGCS 109

Title: Perfect score: us-09-754-826<sub>7</sub>2 628 DFGLDCDEHSTESRCCRYPL....

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

earched:

Total number of hits satisfying chosen parameters: 283138

283138 seqs, 96089334 residues

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	247	39.3	370	2 !	I51199	activin beta B sub
2	241	38.4	255	N	I48235	beta-B
ω	241		411	N	в41398	beta-B
4	237.5	7.	115	N	PN0506	beta B
υī	235	•	349	L	WFPGBB	beta-B
6	235	37.4	407	_	A40150	beta-B
7	235	37.4	408	N	S50899	nhibin p
80	234.5	37.3	393	N	I50103	in beta I
9	232.5	37.0	115	N	PN0505	activin beta B-1 c
10	225.5	35.9	207	N	S37618	vgr protein - rat
11	225.5		513	L	вмни6	morphogen
12	223.5	•	510	N	A54798	Vg-1-related prote
13	212.5	•	313	2	I51284	e morphoge
14	212.5	٠	360	N	A29619	Vgl embryonic grow
15	211.5	•	125	N	\$43295	bone morphogenetic
16	211.5	33.7	352	N	JC5366	activin beta C - m
17	211.5	33.7	352	N	S70580	activin beta C pre
18	211.5	•	436	N	B55452	ge-deriv
19	_	٠	373	N	PW0042	activin - fruit fl
20	•	•	413	N	JC4862	a
21	210.5	33.5	424	<u>_</u>	WFPGBA	beta-A
. 22	•		424	_	S31440	inhibin beta-A cha
23	•		424	_	B40905	inhibin beta-A cha
24		•	425		850898	inhibin beta-A cha
. 25	•		425	N	I47072	inhibin beta-A cha
26			426	_	B24248	
27		•	426	N	JH0690	bone morphogenetic
28	209.5		367	N	JC4151	activin beta D cha
29		33.4	431	_	вмни7	bone morphogenetic

A:Molecule type: mRNA
A:Residues: 1-234 <RES>
A:Cross-references: EMBL:X83376; NID:g603571; PIDN:CAA58290.1; PID:g603572
A:Cross-references: EMBL:X83376; NJD:g603571; PIDN:CAA58290.1; PID:g603572
A:Albano, R.M.; Groome, N.; Smith, J.C.
Development 117, 711-723, 1993
A:Title: Activins are expressed in preimplantation mouse embryos and in ES and EC
A:Reference number: 148243; MUID:93321614

cel

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Accession: I48266

inhibin beta-B chain - mouse (fragment)
N;Alternate names: activin bB chain
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence\_revision 01-Aug-1997 #text\_change 16-Jul-1999
C;Accession: I48235; I48266; S31441
R;Ritvos, O.; Tuuri, T.; Eramaa, M.; Sainio, K.; Hilden, K.; Saxen, L.; Gilbert, S.F.
Mech. Dev. 50, 229-245, 1995
A;Tille: Activin disrupts epithelial branching morphogenesis in developing glandular
A;Reference number: I48235; MUID:95344997
A;Accession: I48235

### ALIGNMENTS

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Endocrinology 135, 702-711, 1994
A;Title: Two messenger ribonucleic acids encoding the A;Reference number: 153288; MUID:94307180
A;Accession: 153288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 134,'D',136-255 <ALB>
A;Cross-references: EMBL:X69620; NID:g50147; PIDN:CAA49326.1; PID:g50148
C;Superfamily: inhibin
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activin beta B-2 chain - N;Alternate names: gact :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-7 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M32756; GB:M32757; NID:g204943; PIDN:AAA41438.1; R;Dykema, J.C.; Mayo, K.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Esch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Mol. Endocrinol. 1, 388-396, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:S72477; NID:g619268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-174 <FEN>
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Alternate names: inhibin/activin beta B-chain
c;Species: Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                               GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -HTHLVHQANPRG-SAGP---CCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP-----
                                                                                                                                                               -HTHLVHQANPRG-SAGP---CCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
    - goldfish
                                                                                                                                                                                                                                                                                                        38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.4%; Score 241;
42.4%; Pred. No.
                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                            Score 241; DB 2;
Pred. No. 1.6e-18;
                     (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         with
                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ).6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rat inhibin alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                               Length 411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         common
                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta
                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta-B-subunit
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C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: A40156; C24248; A40156; S10751
R;Mason, A.J.; Berkemeier, L.M.; Schmelzer, C.H.; Schwall, R.H.
Mol. Endocrinol. 3, 1352-1358, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:X03267; NID:g2005; PIDN:CAA27021.1; PID:g2006
C;Comment: The source of this protein is ovarian follicular fluid.
C;Comment: The mature protein is the carboxyl-terminal segment of a precursor polypep ifferent forms of inhibin have been isolated (A and B) that differ in the amino-termi C;Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of fol C;Superfamily: inhibin C;Keywords: contraceptive; follitropin inhibitor; glycoprotein; gonad F;1-234/Domain: propeptide (fragment) #status predicted <PRO>F;235-349/Product: inhibin beta-B chain #status predicted <MAT>F;35/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                      RESULT 6
A40150
inhibin beta-B chain precursor - human
N;Alternate names: activin AB chain B
                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                   В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A01394
R;Mason, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemin, Nature 318, 659-663, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibin beta-B chain precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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A; Residues: 1-115 <GEW>
C; Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Cloning and sequencing of goldfish activin A;Reference number: PN0504; MUID:93290666 A;Accession: PN0506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Carassius auratus (goldfish)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PN0506
R;Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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A; Residues: 1-349 < MAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ъ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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                                                                                                                                                                                                                                                                                                           292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 -HTHLVHQANPR----GSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP----- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP---- 56
                                                                                                                                                                                                                                                                                                                                    -HTHLYHQANPR----GSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLECD-GTNGGLCCRQQFYIDFRLIGWNDWIIAPAGYYGNYCEGSCP-AFLAGVPGSASS 58
                                                                                                                                                                                                                                                                                                        FHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA
                                                                                                                                                                                                                                                                                                                                                                                                                GLECDGRT--NLCCRQQFFIDFRLIGWSDWIIAPTGYYGNYCEGSCP-AYLAGVPGSASS 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FHTAVVNQYRMRGMSPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strobeck, C.; Peter, R.E. Commun. 193, 711-717, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.8%; Score 237.5; DB 41.9%; Pred. No. 1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 235; DB 1
Pred. No. 6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Eur. J. Biochem. 226, 751-764, 1994
A; Title: Genomic cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Keywords: glycoprotein; gonad; heterodimer; homodimer; ho:F;1-20/Domain: signal sequence #status predicted <SIG>F;21-292/Domain: propeptide #status predicted <PRO>F;293/Product: inhibin beta-B chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; ACCESSION.
A; Molecule type: mRNA
A; Residues: 55-407 < MA.2>
A; Cross-references: GB: M13437; NID: g186416;
A; Cross-references: GB: M13437; Chen, C.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Activin B: A; Reference number: A; Accession: A40150
                                                                                                                                                                                                                          betaB inhibin precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
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Biochim. Biophys. Acta 1039, 135-141, 1990
A;Title: Purification and characterization
A;Reference number: S10751; MUID:90304183
A;Accession: S10751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type:
A; Residues: 1-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 2cen-2c
C; Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 293-294, 'GX', 297-302, 'XX', 305-307
C; Comment: Activins A and B are homodimers of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 22-46, 'A', 48-407 <FEN>
A; Cross-references: GB: M31632
A; Molecule type: DN/
A; Residues: 1-408 < 
A; Cross-references:
                                                               A; Status: preliminary
                                                                                   y DNase I footprinting.
A; Reference number: S50897;
A; Accession: S50899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB: INHBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bin beta-A and beta-B, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: C24248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Title: Characterization and regulation of Reference number: A40156; MUID:89295443; Accession: A40156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feng, Z.M.; Bardin, C.W.; Chen,
ol. Endocrinol. 3, 939-948, 1989
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293
                                                                                                                                                                                                                                                                                                                                                                                    350 FHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA 407
                                                                                                                                                                                                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                              Genomic cloning and sequence analyses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLECDGRT--NLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCP-AYLAGVPGSASS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-407 <MAS>
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er: A40150; MUID:90114200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                          <OHT>
    EMBL: U16240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                         -GSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                         MUID:95112839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 235; DB
Pred. No. 7e-1
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235; L. Yo. 7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.M.; Schwall, R.H.; Mason, A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:AAA59169.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          testicular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <SCH>
inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant
                                                                                                                                                of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 407;
                                                                                                                                                bovine alpha-,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIDN:AAA59451.1; PID:g386827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-subunit mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inhibin beta-B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vitro activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             109
                                                                                                                                                beta(A)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liegeois,
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                                                                                                                                                  and beta
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GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP-----

Query Match Best Local

Matches

1 Similarity 47; Conser

Conservative

16;

Score 232.5; DB 2; Pred. No. 3.6e-18; 6; Mismatches 41;

Indels Length 115;

13;

Gaps

5

56

37.0%;

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C;Date: 13-Sep-1996 #sequence_revision C;Accession: I50103 R;Wittbrodt, J.; Rosa, F.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ър
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 151/1
C; Superfamily: inhibin
                                                                              K;Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E. Biochem. Biophys. Res. Commun. 193, 711-717, 1993 A;Title: Cloning and sequencing of goldfish actives.
                                                                                                                                        C;Species: Carassius auratus (goldfish)
C;Date: 31-Dec-1993 #sequence_revision
C;Accession: PN0505
                                                                                                                                                                                                                                                                                                                                                                       Вb
                                                                                                                                                                                                                                                                                                                                                                                                        δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: ZactbetaB
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
A; Molecule type: DNA
A; Residues: 1-115 <GEW>
C; Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Disruption of mesoderm and axis A; Reference number: I50103; MUID:95011555 A; Accession: I50103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activin beta B - zebra fish
C; Species: Brachydanio rerio (zebra fish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
I50103
                                                                   A; Reference number: PN0504; MUID: 93290666
                                                                                                                                                                                                             activin beta B-1 chain -
                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-393 <WIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes Dev.
                                                  A; Accession: PN0505
                                                                                                                                                                                              N; Alternate names: gact
                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                        336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 FHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 GLECDGRT--NLCCRQQFFIDFRLIGWNDWIIAPTGYYGNYCEGSCP-AYLAGVPGSASS 350
                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 -HTHLVHQANPR----GSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                          w
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                                                                                                                                                                                                                                                                                                                                                                                                        GLDCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP----- 56
                                                                                                                                                                                                                                                                                                      FHTAVVNQYRMRGMSPGSVNSCCIPTKLSTMSMLYFDDEVNIVKRDVPNMIVEECGCA
                                                                                                                                                                                                                                                                                                                                     "HTHLVHQANPR----GSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                       GLECDGNN-GGLCCRQQFYIDFRLIGWNDWIIAPAGYYGNYCEGSCP-AYMAGVPGSASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lt, J.; Rosa, F.M.
8, 1448-1462, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
47; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 39.8
47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: X76051; NID: g516356; PIDN: CAA53636.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.4%;
                                                                                                                                                                                                               goldfish (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 234.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 235; DB 2
Pred. No. 7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                            31-Dec-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-Sep-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         formation
                                                                                       activin
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.7e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
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                                                                                       subunit genes:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ectopic expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:g516357
                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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                                                                                                                                                              17-Mar-1999
                                                                                       Strong
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                                                                                                                                                                                                                                                                                                        393
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                                                                                       structural
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108

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A;Cross-references: GDB:127596; OMIM:112266
A;Map position: 6pter-6qter
C;Superfamily: inhibin
C;Keywords: bone; glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-374/Domain: propeptide #status predicted <PRO>F;34-374/Droduct: bone morphogenetic protein 6 #status
F;241,269,386,404,454/Binding site: carbohydrate (Asn) (
 멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Sauermann, U.; Meyermann, R.; Schluesener, H.J.
J. Neurosci. Res. 33, 142-147, 1992
A;Title: Cloning of a novel TGF-beta related cyto.
A;Reference number: $37618; MUID:93085758
A;Accession: $37618
                                 δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-207 <SAU>
):Cross-references: EMBL: X58830;
;Note: the sequence from Fig. 4
;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-1994 #sequence_revision 26-May-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
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                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A39263;
A; Accession: B39263
Molecule type: mRNA
Residues: 1-513 <CEL>
                                                                                                                                                                                                                                                                                                                                                                                                                  R;Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
A;Tille: Identification of transforming growth factor beta family members presa, Reference number: A39263; MUID:91088608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                            A; Gene: GDB:BMP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: B39263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone morphogenetic protein 6 precursor - human

    Matches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary
                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:M60315;
 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 QTLVHLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96
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DYNSSELKTACRKHELYVSFQDLGWQDWITAPKGYAANYCDGECSFPLNAHMNATNHAIV 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --LVHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYNSSELKTACKKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCDEHSTESRCCRYPLTVDFEAFGW-DWITAPKRYKANYCSGECEFVFLQKYPHTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -HTHLVHQANPR----GSAGPCCTFTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLECD-GINGGLCCRQQFYIDFRLIGWNDWIIAPAGYYGNYCEGSCP-AYMAGVPGSASS 58
                                   DCDEHSTESRCCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYPHTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FHTAVVNQYRMRGISPGSVNSCCIPTKLSTMSMLYFDDEYNIVKRDVPNMIVEECGC
                                                                       Similarity 41.46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S37618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.9%;
                                                                                          35.9%;
                                                                                                                                                                                                                                                                                                                                              GB:M38694; NID:g339561;
                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NID: 957475; PIDN: CAA41634.1; PID: 957476 is inconsistent with that from Fig. 1 in
                                                                     Score 225.5;
Pred. No. 9.7e
l3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 225.5; DB 2
Pred. No. 3.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                        225.5; DB 1
No. 9.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine,
                                                                                                           DB 1;
                                                                         45;
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                                                                                                                                                             (covalent)
                                                                                                                                                                                                                                                                                                                                                PIDN: AAA36737.1;
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                                                                                                       Length
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                                                                       Indels
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                                                                                                            513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207;
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                                                                                                                                                               #status
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                                                                       Gaps
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bone morphogenetic protein-7 - chicken (fragment) (Species: Gallus gallus (chicken) (c;Species: Gallus gallus (chicken) (c;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 (c;Accession: I51284 R;Houston, B.; Thorp, B.H.; Burt, D.W. J. Mol. Endocrinol. 13, 289-301, 1994 A;Reference number: I51284; MUID:95200473 A;Reference number: I51284; MUID:95200473 A;Accession: I51284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
C;Accession: A54798; A33925; S47442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA A;Residues: 'M',74,'K',76-85,'P',87-510 <LYO> A;Cross references: GB:J04566; NID:g202352; PC;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lyons, K.; Graycar, J.L.; Lee, A.; Hashmi, S.; I
Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989
A;Title: Vgr-1, a mammallan gene related to Xenopu
A;Reference number: A33925; MUID:89282810
A;Accession: A33925
                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-313 <HOU>
A; Cross-references: GB:
C; Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Gitelman, S.E.; Kobrin, M.S.; Ye, J.Q.; Lopez, A.R.; J. Cell Biol. 126, 1595-1609, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-510 <GIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Recombinant vgr-1/BMP-6-expressing tumors induce A; Reference number: A54798; MUID:94375533
                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X80992; NID:g530729; PIDN:CAA56917.1; PID:g530730 R;Lyons, K.; Graycar, J.L.; Lee, A.; Hashmi, S.; Lindquist, P.B.; Chen, E.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A54798
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                                               Matches
                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 -- LVHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGLD--CDEHSTESR--CCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKYP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --LVHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYNGSELKTACKKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIV 458
                                               48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                               Conservative
                                                                 33.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.6%;
                                                                                                                                                                           NID:g957233;
                                             14;
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                                                                 Score
Pred.
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Pred. No. 1.6
                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                              04-Sep-1997 #text_change 16-Jul-1999
                                                                 212.5;
No. 1.5
                                                                                                                                                                                                                                                                                                         of bone morphogenetic
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                                                                 .5e-15;
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                                               44;
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                                               Indels
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195

FGMSNIAENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFP-LNSYM

-HLVHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGC

108

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A,Gene: Gdf6
C:Superfamily: inhibin
F:1-5/Domain: polybasic protease recognition site #status predicted <PPR>
F:1-5/Product: bone morphogenetic protein homolog GDF6 (fragment) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)
N:Alternate names: growth and differentiation factor 6
C:Specias: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000
C:Accession: S43295
R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee,
Nature 368, 639-643, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vg1 embryonic growth factor - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 21-Jul-2000 C;Accession: A29619
                                                                                                                                                                         Qy
                                                                                                                                                                                                                            Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Limb alterations in brachypodism mice due R;Reference number: S43294; MUID:94195427 A;Accession: S43295
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A;Accession: A29619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Weeks, D.L.; Melton, D.A. Cell 51, 861-867, 1987
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Search completed: May 20,
Job time: 45 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-125 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U08338; NID:g488463; PIDN:AAA18779.1; PID:g488464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GB:M18055; NID:g214179; PIDN:AAA49727.1; PID:g214180
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 42; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 33.8%; Score 212.5; DB 2; Best Local Similarity 39.3%; Pred. No. 1.8e-15; Matches 42; Conservative 13; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 HSIEPEDIPLPCCYPTKMSPISMLFYDNNDNVVLRHYENMAVDECGC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 NATNHAIVQTLVHFINPETVPKPCCAPTQLNAISVLYFDDSSNVILKKYRNMVVRACGC 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 HQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGC 108
                                                                                                                                                                                                                                  16 HGKKSRLRCSRKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQT 75
                                                                                                                                                                                                                                                          9 HSTES--RCCRYPLIVDFEAFGW-DWIIAPKRYKANYCSGECEFVFLQKY-PHTH-----
                                                                                                                              LMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGC 124
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                   33.7%; Score 211.5; DB 2; Length 38.5%; Pred. No. 7.6e-16; tive 19; Mismatches 39; Indels
                        2002, 09:21:10
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Result
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                    Score
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length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
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                                                                                                                                                                                                                                                                                    Length
    109
126
126
126
126
130
130
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    15
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  AAB20141
AAW63161
AAW69883
AAY15386
AAB73182
AAB73189
AAB20153
AAB720153
AAB20153
                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (without alignments)
398.520 Million cell updates/sec
Chicken GDF-8. Ga
Growth differentia
Turkey growth diff
Human growth diffe
                                                                                                                                                                                                                                                                                 Description
                                                                                    Growth differentia
                                                                                                                 Murine GDF-8
Rat GDF-8. 1
                                                                                                                                                                                Human growth diffe
Mouse growth diffe
Murine growth diff
                                                                                                                                                               C-terminal
                                                                                                                                            region
-8 #1.
                                                                                                                    Rattus
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#### AAB20141 RESULT 30-APR-2001 AAB20141; AAB20141 standard; Protein; 109 --(first entry) ć

ALIGNMENTS

Human growth differentiation factor 8 C-terminal region

Growth differentiation factor 8; GDF-8; myostatin; down-regulation; vaccine; muscle; meat; cachexia; cardiant; human; mutant; mutein.

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20-JUL-1999;
26-JUL-1999;
                                                           WO200105820-A2
                                                                  Synthetic
                           (MEBI-) M & E BIOTECH AS
                                            20-JUL-2000; 2000WO-DK00413
                                                    25-JAN-2001
                                  99DK-0001014.
99US-0145275.
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Increasing the muscle mass of animals used in meat production by down regulating growth differentiation factor 8 (GDF-8) activity in the animal through induction of anti-GDF-8 antibody production  $\,$ 

WPI; 2001-112680/12.

Halkier T,

Mouritsen

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RESULT
AAR63161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence comprises the 109 amino acid residue
CC C-terminal region of human growth differentiation factor 8
(GGDF-8), i.e. residues 267-375 of the full-length protein (see
CC AAB20131). The homodimer of this region is thought to be the
CC biologically active form of GDF-8. It is an object of the
CC biologically active form of GDF-8. It is an object of the
CC invention to produce a recombinant therapeutic vaccine capable of
CC growth rate of farm animals. Variants of GDF-8 (see AAB20145-53)
CC are provided that are capable of breaking autotolerance against
CC growth rate of farm animals. Variants of GDF-8 (see AAB20145-53)
CC are provided that are capable of breaking autotolerance against
CC growth rate of farm animals. Variants of GDF-8 (see AAB20145-53)
CC are provided that are capable of breaking autotolerance against
CC growth rate of farm animals. Variants of CDF-8 (see AAB20145-53)
CC are provided that are capable of breaking autotolerance by a
CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
CC T-cell epitope can be
CC region limits the possible sites in which the T-cell epitope can be
CC positioned without major disturbance of the native 3-dimensional
CC positioned without major disturbance of the native 3-dimensional
CC can be used for genetic immunisation of the animals. Down-regulation
CC cattle, pigs and poultry used for meat production, reducing the need
CC for antibiotic feed-additives. Anti-CDF8 vaccines can be used to
C treat human diseases such as cancer cachexia where muscle atrophy is
C pronounced and for nationals suffering from a which the protein there's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 108
                Q-PSDB;
                                                                            Lee
                                                                                                                                                                                                                                                                                                                                               Growth differentiation factor-8; GDF-8; cell proliferation; adipocyte; obesity; transforming growth factor-beta.
                                                                                                                                                                                                                                                                                                                                                                                                         Mouse growth differentiation factor-8 partial sequence
                                                                                                                                                        19-MAR-1993;
                                                                                                                                                                                              18-MAR-1994;
                                                                                                                                                                                                                                    29-SEP-1994
                                                                                                                                                                                                                                                                           WO9421681-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR63161 standard; Protein; 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED
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                                    1994-316943/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108;
                  Q76380
                                                                            Mcpherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and for patients suffering from acute and chronic heart
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                                                                                                                                                        93US-0033923
                                                                                                                                                                                              94WO-US03019
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Pred. No. 1.3e-59;
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Best Local
                                                                                                                                                            23-MAY-1997;
05-FEB-1997;
28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New growth differentiation factor \theta - useful for treatment and diagnosis of cell proliferative disorders esp. of muscle.
                                              Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contents, also use of GDF-8 inhibitors for treating cancer, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDF-8 can
                   Example
                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                     Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDF-8 can be used to maintain cells before transplantation; to improve efficiency of cell fusion and to treat obesity or diseases related to abnormal adipocyte proliferation.
                                       neuromuscular disease
                                                                                       N-PSDB; AAV45809
                                                                                                                       Lee
                                                                                                                                          (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                      05-FEB-1998;
                                                                                                                                                                                                                          06-AUG-1998
                                                                                                                                                                                                                                             W09833887-A1
                                                                                                                                                                                                                                                                                                                            Mus sp
                                                                                                                                                                                                                                                                                                                                              therapy.
                                                                                                                                                                                                                                                                                                                                                                                                Murine growth differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW69883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW69883 standard;
                                                                                                                                                                                                                                                                                                                                                           neuromuscular
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                                                                                                                                                                                                                                                                                             leavage-site
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                                                                                                  1998-437444/37.
                                                                                                                                                                                                                                                                                                                                                        differentiation factor-8; GDF-8; mouse; transgenic animal;
orming growth factor-beta; muscle; meat; inhibitor; obesity
uscular disease; muscular dystrophy; cachexia; AIDS; cancer
                  2; Page 58; 125pp;
                                                                                                                       McPherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                              97US-0847910
                                                                                                                                                                        97US-0862445.
97US-0795071.
                                                                                                                                                                                                      98WO-US02479
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17..126
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 pp;
                                                                                                                                                                                                                                                               "mature polypeptide"
                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 622; DB 15;
Pred. No. 1.6e-59;
                                                                                                                                                                                                                                                                                                                                                                                                factor-8 C-terminal fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 126;
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This

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amino acid sequence of the

C-terminal portion

of mouse

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GC, GDF-8 expression is disrupted or interfered with. Also claimed CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb CC from these animals; (2) method for increasing muscle mass in CC animals by administering an antibody (Ab) that binds to GDF-8; (3) CC inhibiting the action of GDF-8 by treating feetal or adult muscle CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic CC acid encoding a GDF-8 protein truncated by loss of the C-terminal CC active fragment. The transgenic animals have increased muscle mass of the case of the contents of the contents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                       growth differentiation factor; tissue growth; muscle growth; cell differentiation; animal feed; muscle disorder; bone degeneration; nerve degeneration; GDF-8; development; transforming growth factor beta; TGF-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY15386 standard; Protein; 126
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                     05-FEB-1999;
                                                                         12-AUG-1999
                                                                                                                                                                                                                            Cleavage-site
                                                                                                                                                                                                                                                                                Cleavage-site
                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY15386;
                                                                                                                       WO9940181-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dfgldcdehstesrccrypltvdfeafgwdwiiapkrykanycsgecefvflqkyphthl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vhqanprgsagpcctptkmspinmlyfngkeqiiygkipamvvdrcgcs 126
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                     99WO-US02511.
                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                               /label= Potential_proteolytic_cleavage_site
16..17
                                                                                                                                                                                              /label= Potential_proteolytic_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.0%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse Growth Differentiation Factor-8 (GDF-8).
                                                                                                                                                                           "cleavage generates mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 1
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.6e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or monitoring),
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RESULT
AAB73182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursor protein. The predicted GDF-8 sequence contains two potential C proteolytic processing sites.

CC cleavage of the precursor at the second of these sites would generate a mature C terminal fragment 109 amino acids in length with a predicted concept and the predicted concept and the predicted concept and the proteolytic follows to result in increased bone and muscle mass (such as ribs) when expressed in reduced amounts. GDF-8 minus transgenic canimals and forms of animal feed that can inhibit/reduce production of GDF-8 are of commercial interest.

CC of muscle bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8 cantisense molecule or dominant negative polypeptide could be used with foetal or adult muscle cells, bone cells or progenitor cells. These agents can be administered to a patient suffering from a disorder such cas muscle wasting disease, neuro muscular disorder, muscle atrophy, cell disorders, and aging for example.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                      Gene therapy; growth differentiation factor-8; GDP-8; AIDS; cachexi neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculodegenerative disease; tissue repair; muscle wasting disease; neuromuscular disorder; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of the C-terminal region precursor protein. The predicted GDF-8 sequence contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-494289/41.
N-PSDB; AAZ06446.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-1998;
05-FEB-1998;
                                                             22-FEB-2001
                                                                                                              WO200112777-A2
                                                                                                                                                                                                                                               traumatic injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine GDF-8 #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB73182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New differentiation factor useful for treating neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.873182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 dfgldcdehstesrccrypltvdfeafgwdwiiapkrykanycsgecefvflqkyphthl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McPherron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein; 126 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0124180.
98US-0019070.
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                                                                                                                                                                                                                                               congestive obstructive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.0%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 622; DB 20; Pred. No. 1.6e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                               pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                  disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the GDF-8
two potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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17-AUG-2000; 2000WO-US22884

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RESULT
AAB73189
ID AAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to growth differentiation factor-8 (GDF-8) coding sequences and proteins. The present sequence is a GDF-8 protein, which was isolated in the present invention. GDF-8 is useful for treating neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular dystrophy), musculodegenerative diseases or in tissue repair due to trauma, obesity and disorders related to abnormal proliferation of adipocytes. GDF-8 is also useful for treating malignancies of the various organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, spinal cord injury, traumatic injury, congestive obstructive pulmonary disease
                                                                                                                                                                                                                                                                                          neurodegenerative disease; amyotrophic lateral sclerosis; obesi
muscular dystrophy; musculodegenerative disease; tissue repair;
muscle wasting disease; neuromuscular disorder; spinal cord inj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New substantially purified growth differentiation factor-8 polypeptide, useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome and cachexia
                           19-AUG-1999;
                                                                        17-AUG-2000;
                                                                                                                          22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                Gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB73189
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                                                                                                                                                                       WO200112777-A2
                                                                                                                                                                                                                      Rattus
                                                                                                                                                                                                                                                                      traumatic
                                                                                                                                                                                                                                                                                                                                                                                                                  Rat GDF-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (OLYU)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       injury, traumatic injury, (COPD), AIDS or cachexia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
mes 108; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dfgldcdehstesrccrypltvdfeafgwdwiiapkrykanycsgecefvflqkyphthl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vhqanprgsagpcctptkmspinmlyfngkeqiiygkipamvvdrcgcs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-211209/21.
DB; AAF63547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McPherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                   injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.0%;
ilarity 99.1%;
Conservative
                                                                          2000WO-US22884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                growth differentiation factor-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                           99US-0378238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0378238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124pp; English.
                                                                                                                                                                                                                                                                      congestive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 622; DB
; Pred. No. 1.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130
                                                                                                                                                                                                                                                                      obstructive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                   pulmonary
                                                                                                                                                                                                                                                                                                                                                                GDF-8; AIDS; cachexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126
                                                                                                                                                                                                                                                                                                                                       obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
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  ACC CONTRACTOR OF THE THEFT THE THEFT THEF
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AAB20153
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to growth differentiation factor-8 (GDF-8) coding sequences and proteins. The present sequence is a GDF-8 protein, which was isolated in the present invention. GDF-8 is useful for treating neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular dystrophy), musculodegenerative diseases or in tissue repair due to trauma, obesity and disorders related to abnormal proliferation of adipocytes. GDF-8 is also useful for treating malignancies of the various organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, sphal cord injury, traumatic injury, congestive obstructive pulmonary disease (COPD), AIDS or cachexia.
                                                                                                                                                                                            Chimeric
Chimeric
                                                                                                                                Key
Region
                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                      T-cell epitope;
cardiant; human;
                                                                                                                                                                                                                                                     Growth differentiation factor 8; T-cell epitope; down-requilation.
                                                                                                                                                                                                                                                                                                 Growth differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dystrophy, nand cachexia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee
                           Region
                                                       Region
                                                                                     Region
                                                                                                                                                                                                                                                                                                                              30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                         AAB20153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 9; Fig 2; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New substantially purified growth differentiation factor-8 polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-211209/21.
DB; AAF63555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
108; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating muscle wasting disease, obesity, muscular only, neuromuscular disorder, acquired immunodeficiency syndrome shexia
                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                            Homo sapiens.
Clostridium tetani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                              (first entry)
                          /note= "
52..160
                                                         /note=
37..51
                                                                                       16..36
                                                                                                                                              Location/Qualifiers
                                                                                                                   /note=
             /note=
                                                                                                                                                                                                                                       mutant;
                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.0%;
99.1%;
                                                                                                                                                                                                                                                                                                  factor 8 AutoVac construct GDF-8 ext
                                         "tetanus toxoid P2 epitope"
                                                                     "tetanus toxoid
                                                                                                     "identical to GDF-8"
"identical
GDF-8"
                                                                                                                                                                                                                                         mutein
                                                                                                                                                                                                                                                                                                                                                                                           160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 622; DB Pred. No. 1.6e 0; Mismatches
                                                                                                                                                                                                                                                                   GDF-8; myostatin; tetanus toxin;
                                                                                                                                                                                                                                                       vaccine;
            ç
            residues 267-375
                                                                                                                    residues 215-230 of
                                                                       P30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
l.6e-59;
les 1;
                                                                                                                                                                                                                                                       muscle;
                                                                       epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 130;
                                                                                                                                                                                                                                                       meat; cachexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
             of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130
               human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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RESULT
AAB73188
ID AAB7
XX
AC AAB7
XX
DT 11-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of AutoVac construct GDF-8 ext, which consists of the C-terminal 160 amino acids of human growth CC differentiation factor 8 (GDF-8, see AAF20131) with residues 16-36 CC substituted by the promiscuous tetanus toxin T-cell epitope P30 (see AAB20144) and residues 37-51 substituted by tetanus toxin T-cell cell cepitope P2 (see AAB20143). It is an object of the invention to CC produce a recombinant therapeutic vaccine that is capable of effecting CC down-regulation of GDF-8 in order to increase the muscle growth CC rate of farm animals. The vaccines (see AAB20145-53) are capable of the C-terminal portion of human GDF-8 in which a portion of the CC the C-terminal portion of human GDF-8 in which a portion of the CC native sequence is replaced by a T-cell epitope such as P30, with CC minimal disturbance of the authentic 3-dimensional structure of CC the protein. Nucleic acids encoding the GDF-8 variants can be used CC activity can increase muscle mass by up to at least 45% in cattle, CC pigs and poultry used for meat production, reducing the need for antibiotic feed-additives. Anti-GDF8 vaccines can be used to treat human diseases such as cancer cachexia where muscle atrophy is concerned and for nationts suffering from activate and chronic heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                               11-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Increasing the muscle mass of animals used in meat production by deregulating growth differentiation factor 8 (GDF-8) activity in the animal through induction of anti-GDF-8 antibody production \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                            AAB73188;
                                                                                                                                                  AAB73188 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 107-108; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEBI-) M & E BIOTECH AS
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26-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-2001
                                                                                                                                                                                                                                                                                                             112
                                                                                                                                                                                                                                                                                             52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                         2001-112680/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 99.1
08; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouritsen S,
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99DK-0001014
99US-0145275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Cys-124 may be substituted by Ser to avoid
disulfide bond formation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patients suffering from acute and chronic heart
                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.0%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "optionally replaced by Glu-Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klysner S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 622; DB 2
Pred. No. 2e-59;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            111
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New substantially purified growth differentiation factor-8 polypeptide, useful for treating muscle wasting disease, obesity, muscular dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexi neurodegenerative disease; amyotrophic lateral sclerosis; obesity; muscular dystrophy; musculodegenerative disease; tissue repair; muscular dystrophy; musculodegenerative disease; tissue repair; muscle wasting disease; neuromuscular disorder; spinal cord injury;
                                                                                                                                                                                                                                                                               N-PSDB; AAF63554
                                                                                                                                                                                                                                                                                                                                          (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                  19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-2000; 2000WO-US22884
                                                                                                                                                                                                                                                                                                                                                                                                                  22-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200112777-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        traumatic injury; congestive obstructive pulmonary disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicken GDF-8
                                                                                                                                                                                                                                                                                          2001-211209/21.
                                                                                                                                                                                                                                                                                                                   McPherron AC;
                                                                                                                                                                                                                                                                                                                                                                  99US-0378238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cachexia;
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The present invention relates to growth differentiation factor-8 (GDF-8) coding sequences and proteins. The present sequence is a GDF-8 protein, which was isolated in the present invention. GDF-8 is useful for treating neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and muscular dystrophy), musculodegenerative diseases or in tissue repair due to trauma, obesity and disorders related to abnormal proliferation of adipocytes. GDF-8 is also useful for treating malignancies of the various organ systems, particularly cells in muscle or adipose tissues and in gene therapy for the treatment of cell proliferative or immunological diseases mediated by GDF-8. In addition, GDF-8 is also useful for treating muscle wasting disease, neuromuscular disorder, spinal cord injury, traumatic injury, congestive obstructive pulmonary disease (COPD), AIDS or cachexia.

Example 9;

Fig 2; 124pp; English.

Sequence 226 AA;

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Query Match
Best Local :
 Matches
         Similarity
 Conservative
        99.0%;
99.1%;
 0,
        Score 622; DB 22; Pred. No. 2/9e-59;
 Mismatches
                  Length 226;
Indels
0;
Gaps
0
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В
                             δÃ
                                                             Db
                                                                                         Qy
                                                             118
178 vhqanprgsagpcctptkmspinmlyfngkeqiiygkipamvvdrcgcs
                           61 VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                         1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                          226
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0;

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AAB20152
     RESULT
     9
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AAB20152 standard; Protein;

KXXEX DXXXX

30-APR-2001 (first entry)

Growth differentiation factor 8 AutoVac construct GDF-8 dimer.

factor 8 GDF-8; myostatin; tetanus toxin;

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Query Match
.Best Local S
Matches 108
                                                                                                                                                                                                                                                                                                       recombinant therapeutic vaccine that is capable of effecting down-regulation of GDF-8 in order to increase the muscle growth rate of farm animals. The vaccines (see AMB20145-53) are capable of breaking autotolerance against autologous GDF-8. They comprise the C-terminal portion of human GDF-8 in which a portion of the native sequence is replaced by a T-cell epitope such as P30, with minimal disturbance of the authentic 3-dimensional structure of the protein. Nucleic acids encoding the GDF-8 variants can be used for genetic immunisation of the animals. Down-regulation of GDF-8 activity can increase muscle mass by up to at least 45% in cattle, pigs and poultry used for meat production, reducing the need for antiblotic feed-additives. Anti-GDF8 vaccines can be used to treat human diseases such as cancer cachexia where muscle atrophy is pronounced and for patients suffering from acute and chronic heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of AutoVac construct GDF-8 dimer comprising 2 copies of the 109-amino acid C-terminal region of prowth differentiation factor 8 (GDF-8, see AAF20141) covalently connected through the P2 and P30 T-cell epitopes (see AAB20143-44) of tetanus toxin. It is an object of the invention to produce a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-1999;
26-JUL-1999;
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Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia; cardiant; human; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 105-106; 110pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animal through induction of anti-GDF-8 antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Increasing the muscle mass of animals used in meat production by down regulating growth differentiation factor \theta (GDF-\theta) activity in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200105820-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-112680/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEBI-) M & E BIOTECH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUL-2000; 2000WO-DK00413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                      Local Similarity res 108; Conse
Homo sapiens
Clostridium
                                                                                                                                                                                                                                      254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouritsen S,
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99DK-0001014
99US-0145275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "optionally replaced by Glu-Gly"
235..236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "109 C-terminal residues of human 90..91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-
110..1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125..145
/note= "tetanus toxoid P30 epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..124
                                                                                                                             99.0%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "109 C-terminal residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tetani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "tetanus toxoid P2 epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "optionally replaced by Glu-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klysner
                                                                                                           0,
                                                                                                      Score 622; DB 22; Pred. No. 3.3e-59; 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of human
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDF-8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of human
                                                                                                        0;
                                                                                                      Gaps
                                                      60
       60
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> Q 망

61

VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS

δõ

۰

DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60 dfgldcdehstesrccrypltvdfeafgwdwiiapkrykanycsgecefvflqkyphthl

254

Matches

108;

Conservative

0;

Mismatches

Indels

0

Gaps

0;

313

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RESULT 1
AAB20132
                                                                                                                                                                      da
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of turkey growth differentiation factor 8 (GDF-8), also called myostatin. It is an object of the invention to produce a recombinant therapeutic vaccine capable of effecting down-regulation of GDF-8 in order to increase the muscle growth rate of farm animals. Variants of GDF-8 (GDF-8 (GBF-8 (GBF-8)) are provided that are capable of breaking autotolerance against autologous GDF-8. These comprise a C-terminal portion of human GDF-8 in which a portion of the native sequence is replaced by a T-cell epitope such as the promiscuous tetanus toxin T-cell epitope provided activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to increase muscle mass by up to a least 45% activity is used to in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            animal through induction of anti-GDF-8 antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB20132 standard;
                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MEBI-) M & E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-1999;
26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200105820-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Turkey growth differentiation factor 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-2001
                                                                                                                                                                                                                                                                                      in cattle, pigs and poultry used for meat production, reducing the need for antibiotic feed-additives. Anti-GDF8 vaccines can be used to treat human diseases such as cancer cachexia where muscle atrophy is pronounced and for patients suffering from acute and chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 76-78; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Increasing regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-112680/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUL-2000; 2000WO-DK00413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muscle; meat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the muscle mass of animals used in meat production by growth differentiation factor 8 (GDF-8) activity in the second content of the
                                                                                                                                                                      362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOTECH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99DK-0001014
99US-0145275
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99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is that of turkey growth differentiation factor ad myostatin. It is an object of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ś
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cachexia; cardiant; turkey.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klysner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362
Score 622; DB 22;
Pred. No. 4.9e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                      Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109
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RESULT 12
AAW69888
ID AAW698
XX
AC AAW698
XY
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Chicke
XX
KW Growth
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AAR63160
ID AAR6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                  Growth differentiation factor-8; GDF-8; chicken; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDF-8 can be used to maintain cells before transplantation; to improve efficiency of cell fusion and to treat obesity or diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New growth differentiation factor \theta - useful for treatment and diagnosis of cell proliferative disorders esp. of muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Growth differentiation factor-8; GDF-8; addipocyte; obesity; transforming growth
                                                                                                                                                                          Chicken growth differentiation factor-8.
                                                                                                                                                                                                                                  07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 58; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-316943/39
Q-PSDB; Q76372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human growth differentiation
                                therapy
                                                                                                                                                                                                                                                                                           AAW69888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-1995
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                                                                                                                                                                                                                                                                                                                                           AAW69888 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 vhqanprgsagpcctptkmspinmlyfngkeqiiygkipamvvdrcgcs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dfgldcdehstesrccrypltvdfeafgwdwiiapkrykanycsgecefvflqkyphthl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vhqanprgsagpcctptkmspinmlyfngkeqiiygkipamvvdrcgcs 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcpherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to abnormal adipocyte proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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99.1%;
                                                                                                                                                                                                                                                                                                                                                 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 622; DB 15;
Pred. No. 5.1e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor-8 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                 ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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267

Query Match Best Local Matches 108;

Local

Similarity

99.0%;

Score 622; DB 19; Pred. No. 5.1e-59; 0; Mismatches 1;

Length 375; Indels

0;

Gaps

0

Conservative

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327

61 VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109 ||||||||||||||||| 327 Vhqanprgsagpcctptkmspinmlyfngkeqiiygkipamvvdrcgcs 375

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are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb from these animals; (2) method for increasing muscle mass in animals by administering an antibody (Ab) that binds to GDF-8; (3) inhibiting the action of GDF-8 by treating foetal or adult muscle or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic acid encoding a GDF-8 protein truncated by loss of the C-terminal active fragment. The transgenic animals have increased muscle mass and for poultry reduced cholesterol contents. Method (3) is used to treat muscle wasting or neuromuscular diseases, muscular atrophy and aging, particularly muscular dystrophy, spinal cord or traumatic injuries, congestive or obstructive lung disease, AIDS and cachexia. Method (4) is used to treat cancer of muscle, consective tissue and bone, or obesity. Also (not claimed) GDF-8 can be used to maintain myoblasts intended for transplanting or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAY-1997;
05-FEB-1997;
28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and adipose tissue. The sequence was deduced from a cDNA clone (see AAV45819) isolated from a skeletal muscle cDNA library. The invention provides novel mammalian and avian GDF-8 proteins (see AAW69883-92). A transgenic non-human animal is claimed in which GDF-8 expression is disrupted or interfered with. Also claimed in the contract of the contrac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contentalso use of GDF-8 inhibitors for treating cancer, obesity,
                                                                                          improve efficiency of fusion. Ab can b
quantify GDF-8 (particularly in muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-437444/37
N-PSDB; AAV45819.
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta superfamily that appears to relate to various cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Fig 14c; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuromuscular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the amino acid sequence of chicken growth differentiation factor 8 (CDE-8), a novel member of the transforming growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McPherron AC;
                                                        immunotherapy and
   375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0862445.
97US-0795071.
97US-0847910.
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263..266
267..375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         especially those involving muscle,
                                                        in vivo imaging.
                                                                                      ists intended for transplanting or to
Ab can be used to detect and
n muscle, for diagnosis or monitoring).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA clone
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                                                                                                                                    copies expression is disrupted or interfered with. Also claimed are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb from these animals; (2) method for increasing muscle mass in animals by administering an antibody (Ab) that binds to GDF-8; (3) inhibiting the action of GDF-8 by treating foetal or adult muscle or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic acid encoding a GDF-8 protein truncated by loss of the C-terminal active fragment. The transgenic animals have increased muscle mass and for poultry reduced cholesterol contents. Method (3) is used to treat muscle wasting or neuromuscular diseases, muscular atrophy and gady, particularly muscular dystrophy, spinal cord or traumatic injuries, congestive or obstructive lung disease, AIDS and cachexia. Method (4) is used to treat cancer of muscle, congestive or obstructive lung disease, AIDS and cachexia. Method (4) is used to treat cancer of muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and adipose tissue. The sequence was deduced from a cDNA clone (see AAV45822) isolated from a skeletal muscle cDNA library. The invention provides novel mammalian and avian GDF-8 proteins (see AAW69883-92). A transgenic non-human animal is claimed in which
          can be used to maintain myoblasts intended for transplanting or improve efficiency of fusion. Ab can be used to detect and quantify GDF-8 (particularly in muscle, for diagnosis or monitor also for immunotherapy and in vivo imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contents, also use of GDF-8 inhibitors for treating cancer, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth differentiation factor-8; GDF-8; pig; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity; neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor-8 (GDF-8), a novel member of the transforming growth facto-
beta superfamily that appears to relate to various cell
proliferative disorders, especially those involving muscle, nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 9; Fig 14f; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAY-1997;
05-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of porcine growth differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuromuscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pig growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW69891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1998-437444/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McPherron AC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0862445.
97US-0795071.
97US-0847910.
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Best Local S
Matches 108
                                                                                                                                                                                                                                                                                    23-MAY-1997;
05-FEB-1997;
28-APR-1997;
factor-8 (GDF-8), a novel member of the transforming growth factor beta superfamily that appears to relate to various cell proliferative disorders, especially those involving muscle, nerve and adipose tissue. The sequence was deduced from a cDNA clone (see AAV45810) isolated from a skeletal muscle cDNA library. The invention provides novel mammalian and avian GDF-8 proteins (see AAW65983-92). A transgenic non-human animal is claimed in which
                                                                                                                                   Transgenic animals with gene for growth differentiation factor-8 disrupted - have increased muscle and reduced cholesterol contents, also use of GDF-8 inhibitors for treating cancer, obesity, neuromuscular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth differentiation factor-8; GDF-8; human; transgenic animal; transforming growth factor-beta; muscle; meat; inhibitor; obesity neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                    This is the amino acid sequence of human growth differentiation
                                                                                                                                                                                                                                       Lee
                                                                                                                                                                                                                                                                                                                                                             06-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                    W09833887-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human growth differentiation factor-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW69885;
                                                                                                            Example 3; Fig 5c;
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                                                                                                                                                                                                                                                            (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                     05-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW69885 standard;
                                                                                                                                                                                                             WPI; 1998-437444/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 dfgldcdehstesrccrypltvdfeafgwdwiiapkrykanycsgecefvflqkyphthl 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108;
                                                                                                                                                                                                  AAV45813
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08; Conservative
                                                                                                                                                                                                                                     McPherron AC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375
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                                                                                                                                                                                                                                                                                    97US-0862445.
97US-0795071.
97US-0847910.
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                                                                                                                                                                                                                                                                                                                                    98WO-US02479
                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Asn is N-glycosylated" 263..266 267..375
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 71..73
                                                                                                                                                                                                                                                                                                                                                                                                            /label=
                                                                                                            125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 622;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
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.1e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 375;
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                                                                          growth factor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIDS; cancer;
                                                 nerve
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDP-8 expression is disrupted or interfered with. Also claimed are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb from these animals; (2) method for increasing muscle mass in animals by administering an antibody (Ab) that binds to GDF-8; (3) inhibiting the action of GDF-8 by treating foetal or adult muscle or progenitor cells with a GDF-8 by treating foetal or adult muscle active encoding a GDF-8 protein truncated by loss of the C-terminal active fragment. The transgenic animals have increased muscle mass and for poultry reduced cholesterol contents. Method (3) is used to treat muscle wasting or neuromuscular diseases, muscular attophy and aging, particularly muscular dystrophy, spinal cord or traumatic injuries, congestive or obstructive lung disease, AIDS and cachexia. Method (4) is used to treat cancer of muscle, can be used to maintain myoblasts intended for transplanting or to improve efficiency of fusion. Ab can be used to detect and quantify GDF-8 (particularly in muscle, for diagnosis or monitoring), also for impunchbrary and in vivo imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 108
                                                                                                                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                    Growth differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human growth differentiation factor-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
            muscular wasting, neuromuscular disease,
                         Transgenic animal growth differentiation factor-11 is inhibited insertion of transgene, also use of GDF-11 inhibitors for treating
                                                                          WPI; 1998-447217/38.
                                                                                                                                                                    06-FEB-1997;
                                                                                                                                                                                                 06-FEB-1998;
                                                                                                                                                                                                                               13-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW65460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW65460 standard;
                                                                                                                                     (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 dfgldcdehstesrccrypltvdfeafgwdwiiapkrykanycsgecefvflqkyphthl 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity
108; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunotherapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                    97US-0795671.
                                                                                                                                                                                             98WO-US02310.
                                                                                                                                                                                                                                                                                                        /note= "N-glycosylated" 263..266
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                    factor-8; GDF-8; human.
                                                                                                                                                                                                                                                                                         "RXXR proteolytic cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in vivo imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 622; DB 19;
Pred. No. 5.1e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for diagnosis or monitoring),
              obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                            for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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Search completed: May 20, 2002, 09:21:47 Job time: 82 sec
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                                                                                                                                                                                                                                                                                                                                                                                      Matches 108;
                                                                                                                                                                                                                                                                                                     Best
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of human growth differentiation factor-8 (GDF-8). It shows a high degree of sequence homology to the newly identified human growth differentiation factor-11 (GDF-11, see AAM65458). Alignment of the GDF-8 and GDF-11 sequences reveals potential N-linked glycosylation signals and put-11 served proteolytic processing sites at analogous positions. The 2
                                                                                                                                                                                                                                                                                                                                                                                                                                            proteolytic processing sites at analogous positions. The 2 sequences are related not only in the C-terminal region following the putative cleavage site (90% amino acid sequence identity) but also in the pro-region of the molecules (45% amino acid sequence identity. Claimed transgenic animals in which GDF-11 production is reduced produce higher than normal levels of muscle and are useful in the food industry. GDF-11 polypeptides, polynucleotides and antibodies can be used to modulate GDF-11 activity or gene expression for treatment of cell proliferative disorders involving
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 muscle, nerve and adipose tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 55-56; 89pp; English.
                                                                                                       327 vhqanprgsagpcctptkmspinmlyfngkeqiiygkipamvvdrcgcs
                                                                                                                                                                                            267
                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                 61 VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                              1 DEGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60
                                                                                                                                                                                       dfgldcdehstesrccrypltvdfeafgwdwiiapkrykanycsgecefvflqkyphthl 326
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                   99.0%;
99.1%;
                                                                                                                                                                                                                                                                             0;
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Pred. No. 5.1e-59;
                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                     Length 375;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2002, 09:20:25; Search time 13.12 Seconds (without alignments) 202.926 Million cell updates/sec

Perfect score: Title: 628 US-09-754-826-2

Sequence: 1 DFGLDCDEHSTESRCCRYPL.....KEQIIYGKIPAMVVDRCGCS 109

Searched: 231628 seqs, 24425594 residues Gapop 10.0 , Gapext 0.5

Scoring table:

BLOSUM62

Total number of hits satisfying chosen parameters:

231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	ۍ	4	ω	N	_	Result No.
256	574	574	574	574	574	574	574	574	574	574	574	574	574	574	583	583	611	622	622	622	622	622	622	622	622	622	Score
40.8	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	91.4	92.8	92.8	97.3	99.0	99.0	99.0	9.		99.0	99.0	99.0	99.0	Query Match
52	407	407	407	407	362	362	362	362	126	126	126	126	126	126	108	108	375	376	376	376	375	375	375	375	126	126	Length
1	w	w	2	N	σ	4	Н	Н	ű	4	w	N	۲	_	w	N	ω	W	w	Ν	ω	ω	2	N	w	ω,	BB
US-08-247-907A-4	US-08-795-671-6	US-08-795-671-2	US-08-765-875-6	US-08-765-875-2	PCT-US94-05288-11	US-09-414-234-11	US-08-452-772-11	US-08-247-907A-11	PCT-US94-05288-2	US-09-414-234-2	US-08-795-671-4	US-08-765-875-4	US-08-452-772-2	US-08-247-907A-2	US-09-177-860A-8		US-08-891-789B-2	US-08-891-789B-6	US-09-177-860A-12	US-08-525-596B-12	US-09-177-860A-14	US-08-795-671-5	US-08-765-875-5	US-08-525-596B-14	US-09-177-860A-6	US-08-525-596B-6	ID
	φ,	Ņ	6	Sequence 2, Appli	11,	11,	11,	11,	2,	2,	4,	4,	Sequence 2, Appli	Sequence 2, Appli	8	`	,2	Sequence 6, Appli	12,	12,	Sequence 14, Appl	<u>ر</u>	Sequence 5, Appli	Sequence 14, Appl	Sequence 6, Appli	Sequence 6, Appli	Description

45	44	43	42	41	40	39	38	37	36	35	34	ω G	32	31	30	29	87
235	235	235	235	235	235	235	235	235	235	235	235	235	235	241	256	256	0.07
37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	37.4	38.4	40.8	40.8	40.8
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US-08-525-596B-28	US-08-455-559-24	US-08-581-529B-18	PCT-US94-00685-20	PCT-US94-00666-22	US-08-624-635-20	US-09-172-062-20	US-08-946-092A-20 ·	US-09-153-733A-22	US-08-491-835-20	US-08-481-377-22	US-08-459-214-37	US-08-459-850-37	US-08-197-792-37	US-08-455-550-12	PCT-US94-05288-4	US-09-414-234-4	US-08-452-//2-4
Sequence 28	Sequence 2	Sequence 1	Sequence 20	Sequence 2:	Sequence 20	Sequence 2	Sequence 20	Sequence 27	Seguence 21	Sequence 2:	Sequence 3	Sequence 37	Sequence 37	Sequence 12	Sequence 4,	Sequence 4,	Sequence 4
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### ALIGNMENTS

PATENT NO. 5827733  GENERAL INFORMATION: APPLICANT: Huynh, Thanh APPLICANT: Hee, Se-Jin TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla STATE: CA COUNTRY: US ZIP: 92037 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: Windows Version 2.0 CURRENT APPLICATION NUMBER: US/08/525,596B FILING DATE: 19-SEP-1995 CLASSIFICATION NUMBER: US/08/525,596B FILING DATE: 08-JUL-1994 ATTORNEY/AGENT INFORMATION: NAME: Wetherell, Jr., Ph.D., John R. REGISTRATION NUMBER: 07265/075001 TELEPAN: 619-678-5099 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 126 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal US-08-525-596B-6,
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1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 60

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US-08-525-596B-14
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US-09-177-860A-6
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Sequence 14, Application US/08525596B Pate# t. No. 5827733
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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Patent No. 6096506
                                                                                                                                                                                                                                                                                        Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
                                                                                                                                                                       61 VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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Best Local Similarity
                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619-678-5099 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Wetherell, Jr., Ph.D.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                APPLICANT: LEE, SE-JIN
APPLICANT: MCPHERRON, ALEXANDRA C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US94/07762 FILING DATE: 08-JUL-1994 ATTORNEY/AGENT INFORMATION:
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NUMBER OF SEQUENCES:
                                                                                COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
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                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: CA
                                                                                                                 COUNTRY:
                                                                                                                                     STATE:
                                                                                                                                                       CITY:
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                SOFTWARE:
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ARE: PatentIn Release #1.0, APPLICATION DATA:
                                                                                                                                                     LOS ANGELES
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                                                                                                                                     CALIFORNIA
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1880 CENTURY PARK EAST, FIFTH FLOOR
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25 Executive Square, Suite
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internal
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99.1%;
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                Version #1.25
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

US/08/706,958

FILING DATE:

CLASSIFICATION:

FILING DATE APPLICATION NUMBER:

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US-08-765-875-5
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Best Local Similarity
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FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN PH.D., LISA A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD3641
TELECOMMUNICATION INFORMATION:
                             APPLICATION NUMBER: US/08/795,671
FILING DATE: February 6, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/1060
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                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Se-Jin I
TITLE OF INVENTION:
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               FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: I
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: California
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25 Executive Square, Suite 1400
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619/678-5070
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99.1%;
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                                07265/106001
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Pred. No. 1.2e-65;
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                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 375;
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RESULT 6
US-09-177-860A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION:
US-08-795-671-5
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-09-177-860A-14
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Matches
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                                                                                                         TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                          APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265,
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Huynh, APPLICANT: Lee, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: p
IMMEDIATE SOURCE:
                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 23 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/OFILING DATE: 23-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92121
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                                                  TOPOLOGY:
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                                                                              LENGTH:
                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
unvnh, Thanh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108;
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                                                            : 375 amino acids amino acid
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Pred. No. 1.2e-65;
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US-08-525-596B-12
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Matches 108; Conserv
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Best Local
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 12:
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                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
   4328
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268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 19-SEP-1995
                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLOKYPHTHL 60
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                                                                DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 327
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4225 Executive Square, Suite
                                                                                                                                                                                                                                                                                       376 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                 Ph.D, John R.
                                                                                                                                                                                                                                                                                                                                                                                   07265/075001
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                                                                                                                            Score 622; DB 2; I
Pred. No. 1.2e-65;
0; Mismatches 1;
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Pred. No. 1
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..2e-65;
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                                                                                                                                                            Length 376;
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                                                                                                                                                                                                                      US-08-891-789B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-177-860A-12
                                                                                                                                                                  Patent No. 6103466
GENERAL INFORMATION:
                                                                                                                                                                                     Sequence 6, Application US/08891789B Patent No. 6103466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6096506 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATE 23-OCT-1222
FILING DATE: 23-OCT-1222
CLASSIFICATION: 424
PRIOR APPLICATION DATA: 426
APPLICATION NUMBER: 08/525
APPLICATION NUMBER: 09/525
APPLICATION NUMBER: 09/525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO:
                                                                                                               APPLICANT: Grobet, I TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Huynh, Thank
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANT
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: FRAGMENT TYPE:
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                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                      STATE: Ontari
ZIP: M5L 1A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Haile, Ph.D, Lisa A. REGISTRATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 07265/075003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 92121
                                                  CITY: Toronto
                                                                                                                                                                                                                                                                                                                      61
COUNTRY:
                                                                  STREET:
                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                 Ontario
                                                                Box 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Gray Cary Ware & Freidenrich LLP 4365 Executive Drive, Suite 1600
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                                                                  Commerce Court
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99.1%;
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                                                                Cassels & Graydon
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                                                                                                                                 Double-Muscling in Mammals
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Pred. No. 1.2e-65;
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COMPUTER READABLE

FORM:

CURRENT APPLICATION DATA:

SOFTWARE:

WORD PERFECT

MEDIUM TYPE: Diskette, 3 1/2 inch, COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1

1.4 Mb storage

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TOPOLOGY: US-08-891-789B-2
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US-08-891-789B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                     TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (416) 863-2653 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                APPLICATION NUMBER: US/08/89 FILING DATE: July 14, 1997 ATTORNEY/AGENT INFORMATION: NAME: Hunt, John C. REGISTRATION NUMBER: 36,424 REGISTRATION NUMBER: 36,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                     COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: July 14, 19 ATTORNEY/AGENT INFORMATION: NAME: Hunt, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL 327
                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 376 amino acids TYPE: amino acid STRANDEDNESS: single
                                  STRANDEDNESS:
                                                    TYPE:
                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                   LENGTH:
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Commerce Court West
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Double-Muscling in Mammals
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4, 1997
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US-08-525-596B-8
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Matches 1
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                                                                                                                             Query Match
Best Local Similarity
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Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                    MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                               SEQUENCE CHARACTÉRISTICS:
LENGTH: 108 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US94/07762 FILING DATE: 08-JUL-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Huynh, APPLICANT: Lee, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375
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            61 VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVV 103
                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                             NAME: Wetherell, Jr., Ph.D, REGISTRATION NUMBER: 31,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0: FILING DATE: 19-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                   1 DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQKYPHTHL
                                                     106;
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                                                                                                                Conservative
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                                                                                                                             92.8%;
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97.2%;
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Pred. No. 1.1e-61;
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Pred. No. 2.4e-64;
1; Mismatches 2
                                                                                                                Mismatches
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                                                                                                                                          Length 108;
                                                                                                                Indels
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; MOLECULE TYPE: protein ; FRAGMENT TYPE: internal US-09-177-860A-8
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US-09-177-860A-8
                                                                                                                                                                                                                               US-08-247-907A-2
                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                             Sequence 2, Application US/08247907A Patent No. 5639638-GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                     APPLICANT: WOZNEY, John
APPLICANT: CELESTE, Anthony J.
TITLE OF INVENTION: BMP-11 COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 858-677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/5
FILING DATE: 19-SEP-1995
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                     CORRESPONDENCE ADDRESS
                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Huynh, APPLICANT: Lee, S
                *STREET: 87 Camb:
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                         61 VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVV 103
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REFERENCE/DOCKET NUMBER: 07265/075003
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                                                                                                                                                                                                                                                                                                        66 VHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVV 108
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COUNTRY:
                                                                     ADDRESSEE:
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                                                  87 CambridgePark Drive
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                                                                     GENETICS INSTITUTE, INC
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US-08-452-772-2
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Best Local Similarity 89.0
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2:
                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,907
FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: YARRY TARRY
                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,772
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WOZNEY, John
APPLICANT: CELESTE, Anthony J.
TITLE OF INVENTION: BMP-11 COMPOSITIONS
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TELEPHONE: 617 876-1170
TELEFAX: 617 876-5851
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
NUMBER OF SEQUENCES:
TELEPHONE: 617 876-1170
                                                                                                                                                                                                                                                                                                                                                                                         STREET: 8, Cambridge
                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 02140
                                                  NAME: LAZAR, Steven R
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: GENERAL CONTREET: 87 CambridgePark Drive
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REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: May 20 CLASSIFICATION: 43
                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPGMVVDRCGCS 126
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                                                                                                                                                                                                                                                                                                         Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.4%;
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                                                  32,618
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                                    GI5205-CIP
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Pred. No. 1.5e-60;
7; Mismatches 5;
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; MOLECULE TYPE: protein US-08-765-875-4
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US-08-765-875-4
                                                                                                                                                       TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 91.4%;
Best Local Similarity 89.0%;
Matches 97; Conservative
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       Matches
                                                                                                                                                                                                                                                                CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/08/706,958
FILING DATE:
APPLICATION NUMBER: US/08/272,763
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN PH.D., LISA A.
REGISTRATION NUMBER: P-38,347
REGISTRATION NUMBER: P-38,347
REGERENCE/DOCKET NUMBER: P03641
TELECOMMUNICATION INFORMATION:
TELEFAX: 619/455-5100
TELEFAX: 619/455-510
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INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENCTH: 126 amino acid
TYPE: amino acid
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GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: MCPHERRON, ALEXANDRA C.
APPLICANT: MCPHERRON, ALEXANDRA C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC -DOS/MS -DOS
OPERATING SYSTEM: PC -DOS/MS -DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/765,875
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ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
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TYPE: amino acid
TOPOLOGY: linear
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    Conservative
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                     91.4%;
89.0%;
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Score 574; DB 2; Length 126;
Pred. No. 1.5e-60;
7; Mismatches 5; Indels
  0;
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61 VHQANPRGSAGPCCTPTLMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109
                 77
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78 VQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPGMVVDRCGCS 126

Search completed: May 20, Job time: 22 sec 2002, 09:20:47

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